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FIGURE 141

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCCTGACCTGCTATGCAGACGA
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT
GGAATTTGATGATAATGAAGGAAAACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAA
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACCTGACTGCATTTTGC
TTTGTAGAAAGTTAGATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 142

MAVLVLRRLTVVLGLLVLF LTCYADDKPKDPDDKPD DSGKDPKPDFPKFLSLLGTEI IENAVEFILRSMRSTGFM
EFDDNEGKHSSK

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FIGURE 143

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG
CCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCCCTGCACCTCATGGCTCTGC
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC
TGGAGCTGGGCTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA
ATCCCCACTTTGAGAAGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTGCTCTG
TGCAGAGCCCCAAGGAAGGTCTGTCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGC
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCCACCTGGAAACACATTGGGG
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGAC
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCT
CCAAGGCACTCATTTCCTCCTTCCCCAGCCTCCAATTAGAACAAAGCCACCCACCAGCCTATCTATCTTCCACTGA
GAGGGACCTTAGCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG
ACCTTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTCCTT
CGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAACTGGTCACAAAAG
TCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCA
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTT
TAATAAATAGACGAAACCACG

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FIGURE 144

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGLTGASGKVALL
ELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVPAGEDMRQLADGSMDVVVCTLVLCVS
QSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFMWQQVFEPWTKHIGDGCCLTRETWKDLENAQFSEIQMERQ
PPPLKWLFPVGPHIMGKAVKQSFPSKALICSFPSLQLEQATHQPIYLPRLGT

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FIGURE 145

GTGGGATTATTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGGCAGATGTTGGGGC
TTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAAACTAATATTTATATGACAGAAGAAAA
AGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATA
ACTTCCTCAGCTTGAGCAGTTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCTCAACCTATAGACT
TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTGAAG
ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAATGTGATTTCTACATTG
TTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA
TTGTCAATTTTGACCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT
TAACCTTTGCAAGGTTCTACTTGCCAACTTCTGGTTCCAGCGCAAGAAGGCCATATACATGGATGATGATGTAA
TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATT
GTGATTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA
AAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAACC
TGACGGAATGAAACGACAGAATATACTAACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGT
ATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG
ATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCA
AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTTGGGAAAAATGGT
ATATTCCAGACCCAAACAGGCAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTCAAAACAGAA
TTTGAAGTGTAAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTC
AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGT
CAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTG
AATGACTGGAAAGAAGAAGTATATGGCTAGTTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTA
ATTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTT

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FIGURE 146

MSFRKVNIIILVLAVALFLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGRQEEIPVVAASED
RLGGAIAAINSIQHNTSRNVI FYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLGKVKEDPDQGESMKPL
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVVIIRGAGNQNYIGYLDYK
KERIRKLSMKASTCSFNPGVEFVANLTEWKRONITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTID
PMWNVRLGSSAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 147

GTGTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTTCTCCAAAGCA
AGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTGTATAA
ATGATGTTGACACCCTCCACCGAATTCTAAGTGGAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC
TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTACATTTTCATTT
CATTTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA
GCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGG
CAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA
AAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCC
TCTGGGTGGCTGTGCTGCTGAGCCTGGGAACGTCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGGAATATA
AGCCCTTTTCGGGCATTGCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG
CGTGCCAGCAAATGACTATAGCTGGGGCAGTGCGTTACTTGTATTTCAACAGAAGTAAAAATGATCCTCCTGATC
ATCCCATCCTTTCTGCTCTCTCCATCTCTTCTTCTTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCT
CTGTGGTGAGGATTCCGAGAATCATTGTCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG
CATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCTTGTTCCAAGA
ACTCAAGTCACTTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTCTAGGAAAGGTGTTAGTGGTGTGTT
TCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGG
TAGCTTTTTTTGCCTACTTAGTAGCCCATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTCTGT
GTTTTGCTGTTGATCTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT
TCGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGAGGGAA
CAGAACTCCAGGCCATTGTGAGATAGATAACCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA
TTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCT
TTCCTCAAAA

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FIGURE 148

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDYNLSDTERENMKC
VLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFAILIFFWVLWVAVLLSLGTAG
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIAGAVVTCYFNRSKNDPFDHPILSSLSILFFY
HOGTVVKGSEFLISVVRIPRIIVMYMQLKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFL
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

FIGURE 149

[illegible]

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FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPFVTPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVYG
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFTIVLESKPKKGVITYPSAL
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQE
MDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRA
ISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAV
CRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKF
EISDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSSGGTSTGAAINFALEQLFKKSKPNKRKLMILI
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARHSHFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

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FIGURE 151

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTATGCTTTCCGGCT
GCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCTCAGCACCATGGTGCGCCAGGTCCCAGCGGCTCCGCGCC
AGATCCCGCCCTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTC
AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTGA
AACAAACATTCGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGAGGC
TGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCCTCCAGCCTTTCAGAC
CCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTGAACCCAGGAGAGACCCCTGTCACTGTAC
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGT
GGCCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCCGCAACCACATTGATGTGCT
CACTGGCAAGTGGGTGGCCCAGGACGACGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAGCCATCCGGAACCTACACCCG
CTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCTTGGAGGC
CTACTGGCCTGCTCTTCAGAGCCTCATTGGAGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGT
ATGGAAGCAGTTTGGGGGGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGAGAGAAGCGAGAGGGCTA
CCCACTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACTCTCTAGAACT
CGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGCGGATTTGCAACAATCAAAGATCTGCG
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTTGA
CCCAACCAACTTCATCCACAACATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGATCCTGGG
GGCTGGGGGGTACATCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAA
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTCGAAATTTAGAA
AAACACTGTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTTCTCACCAGAAAACCATGACCA
GGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCCTCTCAGCTGCCCCAGTCAGCCCTTACCTCCAAGTT
GGCATTACTGGGACAGGTTTTCTAGACTCCTCATTAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCT
AAACTATAATAAATTGCTTTTGGCTATCATAAA

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FIGURE 152

MPFRLLIPLGLLCALLPQHGGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN
ASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMVPVFSLEAYWPGLSLIGDIDNAMRTFL
NYTTVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELGRDAVESIEKISKVECGFAT
IKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGLTFSPENHDQARERKPAKQKVPLLSCPSQP
FTSKLALLGQVFLDSS

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FIGURE 153

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCTTCGT
CACTCACCTGTTCTTGCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACG
CCTATTCAGGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTCATCCTGCTGTGAATAT
GCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTTCATGGTGAGCTAAGGAGAGGGTGGTGGCAG
TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAAGTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGT
TAAAAACCTAGAAAGCAAAAGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTCAACTGGGAGCATGTTT
TGAGGGTGCCCTCCCAAGCCTGGGAGTAATATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCTCGTGCT
TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA
CCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTTCCAGAGGAGATACTGGGTGGGAAAAAGATG
GGGCAAAGCGGTATGATGCCTGGCAAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAGCT
CCATGTTTCCTAACAGATTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCATGCACTTTGGGAGGC
CAAGGTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCATCTCTACTAA
AAAAAAAAAATAAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTGAGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTG
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTG
GCCTGGCAGTAATCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSFFNLDEHHPRLEFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGDRRGDVYR
CPVGGAHNAPCAKGLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS
```

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

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FIGURE 155

GCGAGCTCCGGGTGCTGTGGCCCGGCCCTTGGCGGGGCGGCCTCCGGGCTCAGGCTGGCTGAGAGGCTCCAGCTGC
AGCGTCCCCGCCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAAAACAAGCCTGGCAGG
GTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA
GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGAT
ATTTTTCACCCCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAGGT
ACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATGCTAAGATGATGGTAAA
TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGCCTTTCTGAATTGGAGGATTATCTTTCCTA
TGAGACTGTCTTTGAGAATGGCACCAGAACCTTAACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA
AAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAGCATCTT
GGACAAAAGGTTCTTAACCAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCATTCTCAT
TTCCCTTCAGCATGTTCTAAGTGTGCCCACCTGTGTTTCATGATGGAAGGACTATGTCAAAGGGAGTAAAAAGCT
AAGGGTAGGGTTGTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA
AGCTAGTGGTGGTGACCAAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAA
AAAATCTGGCCGGGGTCAGAGGATTGCCGAAGGGAGGCCTTCCTTTTCAGTGGACCCGGGTCAAGAATACCCACAT
TCGGAAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGACTATGACTATGCTCTTCTGGAGCTGAAGCG
TGCTCACAAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAATGCCTGGTGGATGATCCACTT
CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTGCAGTGTGTCCGACGAATCCAATGATCT
CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA
AAAGAATTGGAAGCGCAAAATCATTGCGGTCTACTCAGGGCACAGTGGGTGGATGTCCACGGGGTTTCAGAAGGA
CTACAACGTTGCTGTTGCGATCACTCCCTAAAATACGCCAGATTTGCCTCTGGATTACGGGAACGATGCCAA
TTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACAGCTCTGCTTA
CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAACCTCTGTCAATAGCATTTCACATTTTTCAAATCA
GGAGATTTTTCGTCCTTTAAAAATGTATAGGTGCAGATATTGAACTAGGTGGGCATTCAATGCCAAGTATAT
ACTCTTCTTTACATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTTAA
ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCCTACTCTAAGAAGAAT
CTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA
ATAGAGACAGAAAGTTACAACACAGTTTGTACTACTCTGAGATGGATCCATTTCAGCTCATGCCCTCAATGTTTAT
ATTGTGTTATCTGTTGGGTCTGGACATTTAGTTTGTGTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGC
ATTATAAACAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAATGGGA
GAAATAGTTTTGTTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA
TTTAATAATACTCAAAATATGGACTTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT
GTTGAAAGCCACATTATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTTAGGACAAAGAATTCTGTAA
TCTTTTTCAAGAAAGAGTCTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTG
ATTAGTAATTTTAGATATGTCCTTTCTAAAAATGAATAAAATTTATGAATATGA

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FIGURE 156

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVCGIECQKELPTPSL
SELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRELTNFPFSTAVKL
STGCSGILISPQHVLTAACHVDGKDYVKGSKKL RVGLLKMNRKSGGKKRRGSKRSRREASGGDQREGTREHLQE
RAKGGRRRKKSGRGORIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCSVDESNDLLYQYCD AESGSTGSGVYLRLLKDPDKKNWKRKIIAVYSGHQW
VDVHGVQKDYNAVVRITPLKYAQICLWIHGNDANCAYG

Important features:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

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FIGURE 157

GGGACCCATGCGGCCGTGACCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAGGAGCATGTCCGCG
CCGGGGAAGGCCCGCTCCCGCCGCCATAAGGCTCCGGTCGCCGCTGGGCCCCGCCGCGCTCCTGCCGCCCG
GGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCGCTCGCCCCGAGGCCCGGCCGCGAGCATGGAGCCACCC
GGACGCCGGCGGGGCCGCGCGCAGCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA
GGCGGCGGCCGCGGCCGCGGCCGCGGCCGCTGCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGCAGG
GCGGCGGGCGCCGCGCGAGGGCAAGGTGGTGTGCGAGCAGCCTGGAACCTCGCGCAGGTCTGCCGCCAGATACTCTG
CCCAACCGCAGCGTCACCTGATTCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTTCTGGGTTA
AGTCTCCTTGAAAGATTGGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGACTGTCA
TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACC
CTGGTTCCGCTAAACCTTTCCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTTGGCTCATTA
CGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGATGCATCGCTGGGTAAAGGAG
AAGAACATCACGGTACGGGATACAGGTGTGTTATCTTAAGTCACTGCAGGCCCAACAGTCACAGGCGTGAAG
CAGGAGCTGTTGACATGCGACCTCCGCTTGAATTGCCGCTTTCTACATGACTCCATCTCATGCCAAGTTGTG
TTTGAGGAGACAGCCTTCCTTTCCAGTGATGGCTTCATATATGATCAGGACATGCAAGTGTGTGGTATCAG
GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGAAAAGAACATGATTACAACTGCTCCTTG
ATTGCAAGTGCCCTAACCATTTCTAATATTGAGGCTGGATCTACTGGAAATTGGGGCTGTCATGTCAGACCAA
CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTG
GTAAACAACAAAGGTGACTTCAGATGGCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAAC
ACCCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGC
TTTTGGGCAGATGATGATTATTTCTCGCTGTGAGTATGCAATGATGTCACTAGAGTTCTTTATATGTTAATCAG
ATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACTTT
TCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA
AAAGAGCTAGGTGACGTGATGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCG
CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTTGCTACCTACCGGCTAGCCGGTGGG
GCTCACGTTTATTCAACATATTACCCAAATATTGCTCTGGAAGCTTATGTCACTCAAGTCTACTGGCTTACGGGG
ATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA
GAGGGAACCTGGATAAGCAGCTGAGCTTTAAGTGAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA
TGTTACATTCTGCAATCATTTAAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAA
CCTTATTAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATAACAG
GAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGCCTTTGATTCCCTTTCTTCACATAAAAATATCA
GAAATTACATTTTATACTGAGTGGTATAAATGCAATATACTATTGTTACATGTGAAAAAATTTTATTGACT
TAAAGTTTATTTATTTGTTTTTTGCTCCTGATTTTAAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATC
ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTAATCAAGCAAGC
TGTATATCAAAATTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTTTCATTGAAGCA
AGCAAAATGAAAGCATTTTACTGATTTTAAATTTGGTGCTTTAGATATATTTGACTACACTGTATTGAAGCAA
ATAGAGGAGGCACAACCTCCAGCACCTAATGGAACCACATTTTTTTTCACTTAGCTTTCTGTGGGCATGTGTAAT
GTATTCTCTGCGGTTTTTAACTCTCACAGTACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCC
AGTCATTTTAAATGGCTGCATAATACTGATCCAACAGGTGTTAGGTGTTCTGGTTTGTGTGAGCACTCAATAAA
TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

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FIGURE 158

MEPPGRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP
PDTLPNRTVTILILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSSLKRLDLTNNRIGCLNADIFR
GLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPV
TGVKQELLTCDPPELPSFYMTPSHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIH
NCSLIASALTISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGITAYLQ
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNTNAVATARQLLAYTVE
AANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVMDIASNIMLADERVLWLAQREAKACSRIVQCLQRIATYR
LAGGAHVYSTYSPNIALEAXVIKSTGFTGMTCTVFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKNVSNTFSSL
ALKVCYILQSFKTIYS

Signal peptide:
amino acids 1-33

Transmembrane domain:
amino acids 13-40 (type II)

N-glycosylation site.
amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,
453-457, 592-596

N-myristoylation site.
amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

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FIGURE 159

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTTC
CTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGAAAGTATTTATTGACCAAATTAACAGG
TCTTTGGAGAATTACGAACCATGTTCAAGTCAAACTGCAGCTGCTACCATGGTGTCATAGAAGAGGATCTAACT
CCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATC
ACTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCOCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTG
GAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCAGGTTCCATAATGGATG
GAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTT
TGGGAAGGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTG
GTAAGGTGAGCAGCACAGTGGCCATGGAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCA
GAACGAGATCCTCTCATTTCTTCTGTCTCGGAAAAACCCAAAACTTGTGATGCAGAATACACCAAAAACAGGCC
TGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAG
TATCTGTTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCTGTGTGGCTCACTTGTTTTTC
CATGTTGGTGATGAGTGGCTAGAATTCTTCTATCCACAGCTGAAGCCATGGGGTTCACTATATCCCAGTCAAAACA
GATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGG
GGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATAC
TCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTATTCCCAAATGTTGAAAACGAA
CTATAGTAGTCATCATAGGACCATAGTCTCTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACC
ATAAGCTTGGCTCCTATACCTTGAATATCTGTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAG
AGCAACTCTTGAGAAAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGG
ACCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCACTTTCTTAAGACCAATCACAGCTTGTGCC
TCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTGTCCCATT
TTTGGAGCAGAAAATTCGTCACTTGAAGTAGTACAACCTCATGCTGGAATTGTGAAATTATTCAAGGCGTGATC
TCTGTCACTTTATTTAATGTAGGAAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTTCTCTGAATGGTC
TAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTCTCTTTGTAAAACCATAAACTCTGTTACTCAGGA
GGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATTTCAAGGTTCCCTTTT
GTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

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FIGURE 160

MEWWASSPLRLWLLLFLIPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVIEEDLTPFRGGISRK
MMAEVVRRKLGTHYQITKNRLYREND CMFPSRC SGVEHFILEVIGRI PD MEMVINVRDYPOVPKWMEPAIPVFSF
SKTSEYHDIMYPAWTFWEGGPAVWPIIYPTGLGRWDLFREDLVRSAQWPWKKNSTAYFRGSRTSPERDPLILLS
RKNPKLVDAEYTKNQAWKSMKDTLGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGDWLEF
FYPQLKFWVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSYNVT
RRKGYDQIIPKMLKTEL

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FIGURE 161

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA
CCATGCTCTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTAATTAAGCATGGAATACAGAAAA
CAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATCCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT
GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTCG
CGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCAGTGAATCCCTC
AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTTCTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG
ATAGAACGCGTGAACTGGATGACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACTTCACACTTCGA
GAGCATTCAACTGCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCCACCTTCAGATGTGAAAGCC
AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTA
GGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATA
ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGCATTACAGGTGGGTAACAG
TTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTAT
CTTTTAAACCTAAACCACTCAGAGAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATCTCTATAGAGGATTT
TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTAT
ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTTGAAGATGTT
TATGTCGGGATCTGTTTGAATTTATTAAGGTGAACATTCATATTCCAGAAGACACAAATCTTTCTTTCTATAT
AGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACT
TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGG
ATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACT
GAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGGCCCTTCAAA
GATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAAAACATTTG
GACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA
AACATGTAGAGTTTTTATTATTGAACAATGTAGTCACCTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT
TTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTTTG
GTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTTAAATTAATTTCACTTTGTGTT
TTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAATCATTCTTTACATGCAACATTTTCCAGT
TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAATGTAAAGTCATAGGTCAATTATGATATCAGTA
ATCTCTTGGACTTTGTTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAATCTGAAA

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FIGURE 162

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHFTLREHSNC SH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKDKMLALSLEDEHLLYGDII RQDFLD
TYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPYCSGLGYIMSRDLVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

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FIGURE 163

CATTTCTGAAACTAATCGTGTGAGAAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATATTAACCTTTTTAGG
AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG
TCCTAGTATTAAATTCTTATTGCTTACTGATTTTTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG
AATATAAATAAGAGAAGAAAAAGAATAAAAGTAGATTGAGTCTCCAATTTTATGTAGCTTCAGAAGAAGTGGTT
TGTTTACATGCAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTTG
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGACGCTAGAGCACTTCAGATTCCGTTGCCAA
CTCGTCCCCATTGGTTTCTCTTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC
TTTATACCAGAAAAAGCCAACTATGAATTACTGGAAAAAGAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG
CCAAATTTAAAGCAAAGGGATTGAATCCGGATGGAACCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCT
CCAAGCCATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCACCATCTCCATTAATGTGAAGACAGTCAAAA
AAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA
ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA
ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC
GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGAC
ATGGTCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC
ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAGCAAGC
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCT
TGGTTTTGCCTATCTACAGTGTGATGTATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTT
CTTGAAACCCCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAGAACTATGTTAATTTTTTGCACAT
TAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT
ATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTTATACAGATAAAATTGCAGACACTGT
TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTTGTCTGCATGTGTAAAGATT
TTTACAAGGAAATAAAATACAAATCTTGTTTTTCTAAAAAAGT

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FIGURE 164

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFSGTTEEEIQEICIETLRLYTRKKPNYELLEKE
VEKRRVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSHSESPPRRHHNHGSPHLKAKH
TRDDLKSSNRHGHKRRKRSRSQSRSRDHSDAAKKRHERGHHDRDRERSRSFERSHKSKHHGGSRSRSGHGRHR

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FIGURE 165

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACTGGGCTTA
ATCTGAAGGTTCTCAGTCAAATTTCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGGCTTAAAGGAGCTT
GGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGC
TTCTGTTGTGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCCTGTATT
CAGAACTCTGTAAAGGTGCCTCCCACTACGGCTGACCAAAGATAGGAAGAGGGCGCTCACAAGATGGCTGTCCAG
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAG
ACGAGCCTGGCCTAGACAACCTGCTACGTGCTCCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT
CTGGCCGGAGCAACCGAAGTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA
ATCGAGCTTTGAGTGTTCTTGAAGGACAAAGAGCGGGAGTGCAATTGCCAACCATGCCGACAGGGCAGGGAAA
ATTCTGAAAAACCACTGCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAATTACCAGCA
TCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC
ATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC
TAAAGGTCAACGGGATGGACATCAGCAATGTCCTCACAACACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGG
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGCAGCAGGAACAATGGACAGGCCGCCGGATGCTTACAGAC
CCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAATAAACTGGTGGCA
AGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG
AGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAGTGCGGCTCATCTGATTC
AGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCAGGTTCCGCAGCGGAGCCCTGACATCTTTCAGGAAG
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCTCCATCCTA
CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCGGCATGACCGTCGCAGGGG
GAGCATCACATAGAGAAATGGGATTTGCCTATCTATGTGATCAGTGTTGAGCCCGGAGGAGTCATAAGCAGAGATG
GAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACCTGACAGAGGTGAGCCGGAGTGAGGCAG
TGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG
ACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA
TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG
GCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA
TGATACATGCTTGTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTG
GCACTTTTTTATAGAAATCAATGATGGGTGAGGAAAACAGAAAAATCACAATAGGCTAAGAAGTTGAAACACT
ATATTTATCTTGTGCTGATTTTATATTTAAAGAAAGAATACATTGTAAAAATGTGAGGAAAAGTATGATCATCTAA
TGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTAATACTACTAGTTTTTTTTCAGTGTGGAGGAT
TTCTCATTACTCTACAACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAAACAATAAAATGATTGATT
TGTATACCCCACTGAATTCAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT
GGCCATTTTTTAATTTACAGCTAAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAAT
AAATATTTTTTCAGAAGTTAAA

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FIGURE 166

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPSPEVSAAATIS
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ
GRESENTTAPFVFPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPG
DIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK
LVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDI
FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPYVISVEPGGVI
SRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNNHMAPPDWSF
SWVMWLELPRCLYNCKDIVLRNTAGSLGFCIVGGYEEYNGNKPFIFKSIVEGTPAYNDGRIRCGDILLAVNGRS
TSGMIHACLARLLKELKGRITLTIVSWPGTFL

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FIGURE 167

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCTCAC
AATTTTCATTTCTGTTTTCTGACTTCAAGTTATATACCGTGGAATGGAGTTGATCCCAACCATAACATCGTGGAG
GGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCTTGCAGAGGATTCCACCTTCAAAATCA
TGAACCTCTGGCTGTTGATCAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAGAAGCT
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACATCAA
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAACCTCAAATTGGGAGGCCAACCCACAGAACAGCATT
CTGGGCCAGGCTGTAATCAGAATTGTCGTGTCATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAACACATT
GTGGAGAAGTGATGATACTCTCCCTTACCTTTCCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATT
CCTGTATCATCCTTTTCAATAAAGTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY
SGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

FIGURE 169

[illegible]

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FIGURE 170

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYTIPCCRNEENE
CDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRGQVLRAPKGQILLESYPLNAHC
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLHSDGSKN
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDFGGPVNGYQKITGGPGLI
NGRHAKIGTVVSFFCNSYVLSGNEKRTCQONGEWSGKQPIKACREPKISDLVRRRVLPQVQSRETPLHQLY
SAAFSKQKLQSAPTCKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE
NITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADLKVVLG
KEYRDDDDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
WNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPG
RASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 171

CTGTGCTCTTTTGCTTCAGCCGCGAGTCGCCACTGGCTGCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA
ATCCGTCCTCCACCACCAGATCTTTTCTCCGTGGATTCCCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG
CACCACCATCACAAACCACCACGAGTCATCTTCGGGGCTGGGGTCCCCCATGATCGTGGGGTCCCTCGGGCCCT
GACACGACCCCTGGGTCTCTCTTCGCTGCTGCAGCTGGTGTCTACTCGGTGGCCCTTCTCGCTGGTGGGTAGCGT
GGAGCCCTGGACGGGGTCCATGGGCACTGGTCCATGTTCACTGGTGCTTCTGCTTCTCCGTGACCTGATCAT
CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCT
CTATCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCACCTATGTCCAGTTCCTGTCCCACGGCCG
TTCGCGGGACCACGCCATCGCGCCCACTTCTTCTCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCGT
GACCCGGGCCCGGCCCGGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGTGTGCTGGAGACCTT
CGTTGCTGCATCATCTTTCGCGTTTCATCAGCAGACCCAACTGTACCAGCACCGCCGGCCCTGGAGTGGTGGT
GGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGCT
ACCCATCCCCCTTCCCAGCTTCTGTGCGGGCTGGCCCTTGCTGTCTGTCTCCTCTATGCCACCGCCCTTGTTC
CTGGCCCTCTACCAAGTTTCATGGAAGTATGGCGGCCAGCCTCGCGCTCGAGAGATGTAGCTGCAGCCGCA
CCATGCCCTACTACGTGTGCTGCGTGGGACCGCGCACTGGCTTGCTGGCCATCCTGACGCCCATCAACCTACTGGCGTA
TGTGGCTGACCTGGTGCACCTCTGCCCACTGGTTTTTTGTCAAGGTCTAAGACTCTCCCAAGAGCTCCCGTCCCT
TCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTCTCCGCCCTTTCCTCTGTTTTCT
CTTCTCTGTCTCCCTTCCCTCCCACCTTTTTCTTTCCCTTCCCAATTCTTTCGACTCTAACCAGTTCTTGGATGC
ATCTTCTTCTCTCCCTTCTCTCTTCTGTTTCTTCTCTGTGTGTTTTGTTGGCCACATCTCTGTTTCCACCCCTG
AGCTGTTTTCTTTTTCTTTTCTTTCTTTTCTTTTTTTTTTTTTTAAAGCGGATCTCACTCTGTGGCCAGGCTG
GAGTGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTCAAGCGATTCTCCTCCCCAGCCCTCC
CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTTTTTTCCACTCTCTTTTTTCTCATC
TCTTTTCTGGGTGCTGTGCGCTTCTTATCTGCTGTGTTTGAAGACACCTTCTCCTGTGCTCTTGGGAGCCCT
GAGACTTCTTTCTCTCTTGCTCCACCACCTCCAAAGTGCTGAGCTCACATCCACCCCTTGCAGCCCTCC
ATGCCACAGCCCCCAAGGGGCCCATGCGCAAGACATGCTGCCACCCCTCGCTGTGCTTGTAGTCAGTGTGTAC
GTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCCCAGTGGAGGAA
GGTGTGCAGTGTACTTCCCTTTAAATTAATAAACATATATATATATATATTGGAGGTAGTAATTTCCAATGG
GCGGGAGGCATTAAGCACCCGACCTGGGTCCCTAGCCCCGCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAG
AATTTTTGCCAGGTTACAGAAACCCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTCAT
CCCAACTATTCTCTGTGGTATGAAAAAG

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FIGURE 172

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTIVTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTYVQFLSHGRSRDHAIATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFVACIIFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNL
GECTNVLPPIPFPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 173

[illegible]

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FIGURE 174

MFLATLSFLLPFAHPFGTVSCEYMLGSP LSSLAQVNLS PF SHPKVHMDPNYCHPSTSLHLC SLAWSFTRLLHPPL
SPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALES AFSSYS DLSEGEQEARFAAGVAEQFAIAEAK
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSS
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPL
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:
amino acids 1-15

Casein kinase II phosphorylation site.
amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,
324-328

Tyrosine kinase phosphorylation site.
amino acids 44-52

N-myristoylation site.
amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 11-22

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FIGURE 175

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTGGCACCCCTCCTGC
TCAGTGCGACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCCTTTCAGACAGGACAACCTG
TGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT
CTTCATCTGCAAAATGGGCATAATACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACC
AATACCAAGAAGCCTACAATGTTGGCCTTAGCCAAAATTCGTGTGATTTCACGTTGTTTTATTCACTTCTATC
GGGAGCCATGGAAAAGAAAATCAAGACATAAACACACACAGAACATTGCAGAAGTTTTTAAACAATGGAAAA
TAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAAGAAAATATAACCACCTCAAATCTCAAGGC
GAGTCATTCCCCTCCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGA
GCATTCTTTGGGCAGTCTAAAACCCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTGTTCCTAA
AGTGCCCTTGGAAATGCACCTATAGCAGATGAAGATCTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT
GTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATAACAGTTCCATTACAGTTAG
CATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGGAACCAAGTGGATGGCTTACCACAAA
CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAA
TTCAAAACTCTTTCCAAATACGTAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAAAAGGAAAACGGATTCAAT
TTCCCATCGGCGACTTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACAATGCACCGGAACCTTATGATGT
GAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAATGATTACGCCATGCCAGAAAGTGAAGAAAATGCACG
TGATGGCATTCCATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA
GCAAGTGTCTATCTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTACGTTGGA
TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCCAAAGGTTTTT
TTTCTTACAATTTTTTGCCATCCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTTCTTAGT
AGAAAATATTTGTGGAATCAGATAAACTAAAAGATTTACCATTACAGCCCTGCCTCATAACTAAATAATAAAA
ATTATTCACCAAAAAATTCTAAACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA
CATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT
TTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC
AGGAAAGCTGACCTACCCAGGAAAGTAATAGCTTCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTC
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

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FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISESEANLNSDKENITTSNLKASHSPPL
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHFNATPALSSENFT
WSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFN
TSDPQKENRNTGIVFGAILGAILGVSLTLVGILLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSS
YYNPTLND SAMP ESEENARDGIPMDDIPPLRTSV

Signal peptide:
amino acids 1-23

Transmembrane domain:
amino acids 235-262

N-glycosylation site.
amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,
225-229, 298-302, 307-311

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FIGURE 177

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCCT
GCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGCTTCAACCTGACTTTCCACCTTTTCCTA
CAAATTCGGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGCCACCAGTAACACTTTCGTGGG
TGCCATTCAAGAGATTCCATAAGCAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAA
AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAAGTTGACAACCTGCTCTTCTGTGTCTCCTTACCTCAGAGG
CCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG
CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTGCCTATCCTCGTTCCCCACCGGAACAGAGAGAAACA
CCTGATGTACCTGCTGGAACATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCAATCCA
CCAGGCTGAAGGTAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAA
TTGGGACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA
TCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTTAC
TGCCCTAAGCAGAGAGCAGTTTTCAGGTGAATGGATTCTCTAACAACACTACTGGGGATGGGGAGGCGAAGACGA
TGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAAT
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTTTACACCAAGTGTACAGAGT
CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT
CACAGTGGATTTCTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGCA
ATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTT
TCCTTTTGTATTTTCTTAGCAGAGCTCCTGGTGATGTAGAGTATAAAGCAGTTGTAACAGACAGCTTTCTTAG
TCATTTTGATCATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGA
TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA
GGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA
TACAATACTGTTATTATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAA
GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGGC
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCTTC
CAGTGATGCCACCAGAGAATACATTCTATTAGTTTAAAGAGTTTGTAAATGATTTGTACAAGTAGG
ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAT
GTGAAAAGCAAAA

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FIGURE 178

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTNEASTKKVELD
NCPSVSPYLRGQSKLIEKPDLTLEEVAENPKVSRGRYRPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR
QQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFIHFDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYR
LRYSGYFGGVTALESREQFFKVNFGFSNNYWGWWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE
RMKLLHQVSRVWRDGLSSCSYKLVSVHEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

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FIGURE 179

CGTGGGCGGGGGTCCGCGAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCGCAGTTCTCGAGCTCCAGCTGC
ATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCAATGGCCCCAGGCAGTGTGGTCCGCGCTCGG
CCGCATCCTCTGGCTTGCCCTGCTCCTGCCCTGGGCCCCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCT
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCCTGGTGGCCAAGGACAACGGCAG
CTGGGCCCTGCCCGCTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCCGCTGGTGGCTTACTGGCAAGAT
GGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCCGCCACGTGCCCGGGGAATTCCCGGTCTCTGTCTGGGTAC
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTGGTCTCCCATCACAGAGTTCCCTCGTGGG
GGACCTTGTGTCAACCCAGAACACTTCCCTACCTGGCCAGCTCCTATCTCACTAAGACCGTCTCTGAAAGTCTC
CTTCCTCCCTCCAGACCCGAGCAACTTCTCAAGACCGCCTTGTCTTCTCTACAGCTGGGACTTCGGGGACGGGAC
CCAGATGGTGACTGAAGACTCCGTGGTCTATTATAACTATTCATCATCGGGACCTTCACCGTGAAGCTCAAAGT
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCCTC
GCTGAAGCTGCAGGAAACCCCTTCGAGGCATCCAAGTGTGGGGGCCACCTAATTCAGACCTTCCAAAAGATGAC
CGTGACCTTGAACCTTCTGGGGAGCCCTCCTCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGA
GGAAGGGGAGTGCCACCTGTGTCCGTGGCCAGCAGCGTACAACCTGACCCACACCTTCAGGGACCCCTGGGGA
CTACTGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC
CAGAATCCAGCCGGCTGTCTTGTCTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT
GACCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACCCGGAGCCACCCCTCTGGGGTCAGGTGCTGCTG
CCAGATGTGCTGTGGGCCTTCTTGTCTGGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCT
GCTCCCGCCCTCTATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTTA
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAATTCGCTGGGGCTG
TTGGCCTGGATCATCCATCCATCTGTACAGTTCAAGCACTGCCACAAGCCCTCCCTCTCTGTCAACCCCTGACCC
CAGCCATTCACCCATCTGTACAGTCCAGCCACTGACATAAGCCCACTCGGTTACCACCCCTTGACCCCTTACC
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCGCTGTGACTCCTAGGTGGGCCTGGCTGCCAC
TGCCCATTCCTCTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCCAGACAGCCCTACCT
GTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAATCCATAACTAAAGGTTGTACACATAGATGGGCACA
CTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACACACACAGAAATATAAACACATG
CGTCACATGGGCATTTAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCCTGCACTAGAGC
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCA
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGTGGCTGGCAGGGGCTGGATGGGGGGCAGGACTAATAC
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTGAACTTCACTGAGGAAA
AGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGG
AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCCCTGGCTAACACGGTGAAACCCCGTCTCTACT
AAAAAATACAAAAGTTAGCCGGGCGTGGTGGTGGGTGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA
GAATGGTGCGAACCCGGGAGGCGGAGCTTGAGTGAGCCCAGATGGCGCCACTGCACTCCAGCCTGAGTGACAGA
GCGAGACTCTGTCTCCA

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FIGURE 180

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLYRFHWI
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGFVVLPITEFLVGDVVTQNTSLPWPSS
YLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDTQMVTEDSVVYYNYSIICTFTVKLKVVAEWEEVEPDATRAV
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTILNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN
LTHTFRDEPDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMVENP
EPPSGVRCCCQCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 181

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGCTGGGCCCCTCGGGCCTGACAGATGGCAGTGGC
CACTGCGGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCGCCGGTTTCGTGGGGCCAGGGT
CCAGCGGCTGCGCAGAGGCGGGGACCCCGCCTCATGCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGG
CCTGGGCGCGCCACGGCCGCGGAGCTACTGCGCCTGGGAGCGCGGCTGATCATGGGCTGCCGGGACCGCGCGG
CGCCGAGGAGGCGGCGGCTCAGCTCCGCGCGGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGTCAG
CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT
GCTCCAGGAAGAGCCTAGGCTGGATGCTTGTATCAATAACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGA
AGATGGGTTTGTAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCT
CAAAAGTTTCAGCTCCCAGCAGGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAAGTGGCTAACATTCTTTTACCAG
GGAAGTACCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTGGTATTGTACGGACAAATCT
GGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTCAATTTGGTGTATGGGCTTTTTTCAAACTCC
AGTAGAAGGTGCCCAGACTTCCATTTATTTGGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG
GGATTGTAAAGAGGAAGAAGTGTGGCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGA
AGTGATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAGAGCTGTTTATAAAAGTGCATATCAGTTATATCTG
TGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAATTTTGATATTGGAATAGCCTGCTAAGA
GGTACATGTGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTTAGCAAGATGTTTTAAAT
ATATATAGTAAGTATAATGAATAAAGTACAATGAAAAATACAATTATATTGTAATAATTATACTGGGCAAGCA
TGGATGACATATTAATATTTGTCAGAAATTAAGTACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT
TTCATGGCCAAAGTGTTAACTAGTTTACTACAATGTTTGGTGTGTGTGGAATTATCTGCCTGGTGTGTGCA
CACAAGTCTTACTTGAATAAATTTACTGGTAC

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FIGURE 182

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR
DRARAEAAAGQLRRELQAAECGPEPGVSGVGELIVRELDLASLRSVRAFCQEMLQEEPRLDVLINNAGIFQCPY
MKTEDGFEMQFGVNHGHLNLLNLLGLLKSSAPSRIVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANI
LFTRELARRLEGTVNVTNVLHPGIVRTNLGRHHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK

Important features:**Signal peptide:**

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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FIGURE 183

AACAGGATCTCCTCTTGCACTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCCGAAGATTC
ACTATGGTGAAAATCGCCTTCAATAACCCCTACCGCCGTGCAAAAGGAGGAGGCGCGGCAAGACGTGGAGGCCCTC
CTGAGCCGCACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCC
TCTGGGAGATGTATGCTTACTCTCTTAGGCCCTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATT
TACAAGTACTTCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCAAAAT
TCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTTCGTGAGGATGACAACATTGCA
ATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAGCAATTATTCATGACTTTGAAAAGGGAATG
ACTGCTTACCTGGACTTGTGCTGGGGAACCTGCTATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAA
AATCTGGTAGAGCTCTTGGCAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTA
GTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCC
TTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAAATGCTGGAAGATTAGACAC
TTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGTAAGAGGCAACAGATAGAGTGCTCCTTGGTAATA
AGAAGTCAGAGATTTACAATATGACTTTAACATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCAATTTAC
TCTATTGCTTATGCTTTAAAAAAGGAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTT
TAATTGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTATAGGGTTTAGAT
TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCCGTTGTTTTTTGTTTGTGTTGT
TTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTTAAATTTGAAATATTTTAAATT
GTTTTTGAACTTTTTGTGTAAATATATCAGATCTCAACATTGTTGGTTTCTTTTGTTCATTTTGTACAACT
TTCTTGAATTTAGAAATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGGAATGCACAAAAT
TGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAACCCTATAATAAATTTTACTCTATAC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 184

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQKEGSSGRCLTLLGLSFILAGLIVGGACIY
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDVPVPSFSDSDPAAIHDFEKGMT
AYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLAGRYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNNRKSF
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE
```

Type II transmembrane domain:
amino acids 53-75

N-glycosylation site.
amino acids 166-170

Casein kinase II phosphorylation site.
amino acids 35-39, 132-136, 134-138

N-myristoylation site.
amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 63-74

FIGURE 185

[illegible]

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FIGURE 186

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR
SKCGMCCKT

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FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CATGTTTCCTGTTGCTGCCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCCTCTTACCCT
CCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACAGCTTTACAAGCC
CTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGGAAGGAATGGAGAC
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCCTGGAACCTGCTGAGCAGAACC
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGGTTAGGAGTGCTGATTCGGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT
GCCAATGGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGCAGCGCT
GACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCCATCATACCTC
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG
TGTGATTGAGAGCCATGGTGAAGGCCTGCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTG
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAAGTTTTGAAATTGGAGCCACAGTTTACCCTGTTGCTAT
CAAGTATGACCCTCAATTTGGCGATGCCCTTCTGGAACAGCAGCAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCCTCCCATGACTAGAGAGGCAGATGAAGATGCTGT
CCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCT
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
CAAGGACAGGAGCCGCTCCT**GAG**CCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC
TGGAGTTGCCCGCCGCCCTCCCTGCTGTGTCTTTCCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG
GACTCCGGCTTTCCCGAGCCGCGAGCGGGATCCCTGTGCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGAT
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAG
TGAATCCCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG
GAACTGTCTATCTGCAGGGGCTTTCAGCAAAATGAAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAA
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGCTACTCCAGGCTAACCTG
AACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGGGAATG
GTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGAAGGACACATCACGTTTCA
TGTTTCAAGTACAGGCCCCACAAAACGGGGCACGGCAGGCCTGAGCTCAGAGCTGCTGCAGTGGGCTTTGGATTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

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FIGURE 188

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSTFGIRKLYMKSLKIFAWATLRMERGAKEKNHQLYKP
YTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKG METIMDDEVTKRFS AEELESWNLLSRTN
YNFQYISLRLTVLWGLGVLIRYCFLPLRLAFTGISLLVVGTTVVGYLPNGRFKEEFMSKHVHLMCYRICVRAL
TAIITYHDRENRPNGGICVANHTSPIDVILLASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMF KKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRM
MTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGGLVDLLWDGGLKREKVKDTFKEEQQLYSKMIVGNH
KDRSRS

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FIGURE 189

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACC CGGACCCCTGGCCCTCACGTCTCCTCCAGG
GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCCAGGCTGTTCCCAC
CATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGACGATACCTATGTGGSTTGTGCAGAGGAGATGGAGGAGAA
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCCAACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGAC
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGTCTA
CACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGCGGCGAGGCTCCCGGGAGCTCTA
CATGAGGCACTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG
CTGCAGCAGGGGACCTGGGGAGGTGTTGTTCCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGA
CTCTGTCCGCTTGGGCCAGTTTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCG
GGGCTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAACTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC
TCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAAGTCCAACATCTGCCACTTAGGAGC
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGTTCCGGAC
CCAGCCCTAGCAGCCTTCTCCCCAACCAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTA
TGTGATGGGGACTTCCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTTGCAATGTGGA
GACATGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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FIGURE 190

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEME EKAAPLLKEEMAHHALLRESWEAAQET
WEDKRRGLTLPPGFKAQNGIAIMVYTSSNTLYWELNQAVRTGGGSRELYMRHFPFKALHFYLIRALQLLRGSGG
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKT
LLLAPGEFQLSGVGP

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FIGURE 191

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCCCTCATCTATAT
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCCGTTCCGTTGGTGGGGCCGTGAC
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCAT
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTA
CTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCTCCTGCT
CAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA
GAGAGTGGACATTTGTGCGGAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAGAT
GGAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC
AGTGCACTCCCTAAGTCTCTGCTCA

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FIGURE 192

MAGSPTCLTLIYLWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIVTQN
RNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQOPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT
CCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSS
MVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPA
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTFALSPTSMGPQPTTLG
GPSPTNFDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPKKKYVDQSDRAGGPRAF
SEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:
amino acids 1-25

Transmembrane domain:
amino acids 94-118

N-myristoylation site.
amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,
242-248

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FIGURE 195

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA
CTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGG
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTG
GAGCAAATCCATGTCTTGGAGAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACTATA
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGAAACCTTCCAGCTGATG
GGGCTCTATGGCCGAGAACAGATTTGAGTTCAGACATCAAGGAAAGGTTTGACAACTATGTGAGGAGCATGGA
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAAATGAAGAATGGCCTGA
GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTA
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT
ACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAATTTTTTCATGAAATTATTCCT
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 196

MKMLLLLCGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHG NFRLFLEQIHVLENSLV LKVH
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
RFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 197

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTGAGCCTG
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT
TCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTC
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATG
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTATCCAGAATCC
TTCAACTTGCAAGTGGTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACGACACC
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA
GTATTTTTAGGTCTATTGCTTGTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTATCAGTA
GTTTGAAAAA

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FIGURE 198

MTCCGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR
ACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS
CAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR
SQIV

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FIGURE 199

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC
CGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCT
ACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTC
TGCCACTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGC
TTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

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FIGURE 200

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE
KAIPITPGSATTC

FIGURE 201

[illegible]

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FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT
REAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWQGVPGHSGAWETSGGHGI
FGSQGGGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQ
NEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSS
RGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRRQGVSSNMREISKEGNRLLGGS
GDNYRGQGSWSGSGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:
amino acids 1-21

N-glycosylation site.
amino acids 265-269

Glycosaminoglycan attachment site.
amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.
amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.
amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.
amino acids 301-304

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FIGURE 203

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA
GACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGGCCGCATCCTGGCTT
GGACCTATGCCTTCTATAACAAGTGGCGCCGGCTCCAGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGG
GTCACCTGGGCCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGG
GCTTTACGGTATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCA
ATGCCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATAC
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTGGGATGCTGACGCCCGCCTTCCATTTCAACATCCTGAAGT
CCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA
GTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACA
GCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCC
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC
TGGTGCATGACTTCACAGACGCTGTATCCGGGAGCGGCGTCCGACCCTCCCCACTCAGGGTATTGATGATTTTT
TCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCC
TCTCCTGGGTCCTGTACAACCTTGCGAGGCCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC
TGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCCTTCTGACCATGTGCGTGAAGG
AGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATC
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCT
CCGACGGGCCCAGGAACTGCATCGGGCAGGCGTTCCGCTATGGCGGAGATGAAAGTGGTCTTGGCGTTGATGCTGC
TGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGCCGCCGAGGGCGGGC
TTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCATGACTTTCTGACCCATCCACCTGTTTTTTGCAGATT
GTCATGAATAAAACGGTGCTGTCAA

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FIGURE 204

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLGLITPTEGLK
DSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWLGEIGLLSGGDKWSRHRM
LTPAFHFNIKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATI
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFDVAIRERRRTLPTQGIDDFKDKAKSKTLD FID
VLLLSKDEDGKALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDL
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 205

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT
TTTGCCACAGCAGTTTCTGCAGCTTCCTTGAGGTGTGAACCCACATCCCTGCCCCAGGGCCACCTGCAGGACGC
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTGACGAGTGTTCGTGATC
CTCTTTGCCCTCATCACCATCCTCATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG
CGGGGCGGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGCAAC
AAGACACTGCCCTCTCGGTGCCACCACTGTGTGATTGTGAGCAGCTCCAGCCACCTGCTGGGCACCAAGCTGGGC
CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCACCCACCACTGGCTACTCAGCTGATGTGGGC
AACAAGACCACCTACCGCGTCTGTGGCCCATTCAGTGTGTCCGCGTGTGAGGAGGCCCCAGGAGTTTGTCAAC
CGGACCCCTGAAACCGTGTTCATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCT
GTGATCCAGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGCCGCATGCGGCAATTT
GACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGTTGAGCACAGGCTGGTTTACC
ATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATGGCATGGTCCCCCCCCAACTACTGCAGCCAGCGG
CCCCGCTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGGCCGAGCAATGTGTACCTACATCCAGAAT
GAGCACAGTCGCAAGGGCAACCACACCGCTTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCACGCTGTAT
GGCATCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC
AGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTGCTGGAGTGTCTCCAGCCAATC
AGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCCTGGGGAATCTGTTGGCGAATCAGGGATTGAGGAGT
CTATGTGGTTAATCAGGGGTGTCTTTCTTGTGAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATT
TCTGAGTCAATCTGAGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTGAGAGCCCCAGGAATGGACCCCC
AATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTGCCCCCTCAATTT
CCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAATTTGTGGGTTGTGG
AGGTTGTGGGGGCGTGGGGAGGTCCCAGAGGTGGGAGGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG
GACAAACCCTTCCCCCTCTCTGGGCACCCCTTCTGCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCCTTCCAC
CTCCCCATAAGTGCCCTCGGGTCTGTCTCTCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCTCA
GCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAACTTTAGGGTATTTTTGCGAAACTCCTTCAGG
GTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCTTAGCCCCCTCAGCCAGCTGCCATTAGCTT
GGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCTCTAGCAGGGAGGTTTTCCAAGTGTGGAGGCGCCTTTGGGG
CTGCCCTTTGTCTGGAGTCACTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTCTGGGATGGCTGTCTG
GGAGCTGTATCACCTGGGTTCTGTCCCCTGGCTCTGTATCAGGCACCTTATTAAAGCTGGGCCTCAGTGGGGTGT
GTTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGGACAGATG
GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTGGGTGGGGGCGGTGACTGCCCCAGACTTGGTTTTGTGTA
ATGATTTGTACAGGAATAAACACACCTACGCTCCGGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 206

MSSNKEQSAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVLKKWSITDGYVPILGNKTLPSRCHQCV
IVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRPQEFVNRTPETVFIFWG
PPSKMQKPQGSILVRVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHV
HVGVMVPPNYCSQRRLQRMPIHYEYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:
amino acids 1-29

Transmembrane domain:
amino acids 9-31 (type II)

N-glycosylation site.
amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 50-54

Casein kinase II phosphorylation site.
amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.
amino acids 253-262

N-myristoylation site.
amino acids 37-43, 114-120, 290-294

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FIGURE 207

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCAC
CGCCATGGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTTGG
ATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTTTGTTCTATTTTTTACATCCTTTCACCTATTCCATA
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACTTGCCATCTTTCTTAC
AACGGGCATTGTGTCAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGAGCTTG
TGCACCTGTTCTCACAGGAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAGCAATGA
CGACTTCAGCTGGCAGCAGTGGTGAAGAAATTACTGAACTATTGTCAAATGGACTTCCTGTCAATTTGTTGGCC
ATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTAGGTGCTCC
CTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGCTGAAGGATTAAGGATTTTCTCTTTTGAA
AAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT
TTCCTGTTAGGTTGATTTTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCATTGCAATGGT
TAGGAATTCAGAATTCGCCCGCTCTATTACTGGTCAAGTACATCTTTTCTTAAATATTTTAGCTCCATTA
TTACAAAAAATTATAAAAAAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC
GGTTGGCATACTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAGGGGCCAAGTGTAA
TGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGCTAGACAGATGTTTTGTGGATTGAAAATTTATTTATGG
AATTGCTACAGAGGAGTGTCTTTCTCTCAATTGTTAGAAGAATTTATGTTAACTTTAAGGTAAGGGTGTAAAA
ACATTTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAAGTGTGCAATGTGGGAAGAAATGACATTG
AAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATCAACCTTTTCATGTTTTACC
CTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTGCATCATATATGCCAGAAAAC
CTTCCTCTGCTTCTCTCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAATAACTTTTCAAATATAGTTT
AATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATTCAGAGTGCCCCCTCCCCTGCA
AGGCCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTCATGCATTAACAGTTTAAGATTTAGACC
ATGGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAAGTATTTTTAAGACAAGTTTCTGT
ATACCTCTGAAGTGTGTTTTGATTTTGAGTTCATCATGATAGATCTGCTGTTTCTTATAAAAGGCATTTGTTGTGT
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAATTTCCAGTAAC
CAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAATTATCAGGACTTTTTTCAGGAGTGGGTATAAAAA
CATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATGTTTATTCACTATACATAAAAAATT
ATTTGCCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGTTTTATGAAGTTTATTTCTCAAGAAAATG
GGAATAAATTTGGGATTTGTTCACTTTTTTACTAAAGATGCCATAAGCCACAGGTTTTATTGCCTAACTTAAGC
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGTGGCTGGAGCCTTCCCACTGGAGGC
TGAAAGTGGCTTGTGGTATTATAATGTTTCAAGATTTCAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT
GAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTTTTTTTTTGCAGGAAGTGCATTTCTGGTCTCTC
CCTATTTTCTGTTCTGGATGTGAGTGCAGTGCAGTGCAGTGTCTGTTTATCCACTTGGCCACAGACTTTTTCTAACA
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTGTGCTTTGACCTTGTATACTAGCTTGACATAGT
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTCCATAGAATATGCACTGATACAACATTACCAT
TCTTCTATGGAAAGAAAACTTTTGATGATGAAACAATAAGATTTTAAATATCTATTTTAAAAA

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FIGURE 208

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAIFLT
T
GIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSNDDEFSWQQW

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FIGURE 209

CTTGCAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCACTTGTGTTCTCTCTCCTGGTG
AGAGTTGCAAGCAAGTTTATCAGAGTATCGCCATGAAGTTTCGTCCCCTGCCTCCTGCTGGTGACCTTGTCTCGCC
TGGGGACTTTGGGTGAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCATTTCAGACTGGAGGGA
GAGATTCTGCACTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCGACTGCCGCA
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCCAGCATGTGCCAGGCTTTTGCTGCTGACCCCAAAC
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGTCTAGGCCAT
CCGTGTGCAGGGAGGCTGGACCCCAGGCCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCCAGAGCCCA
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCCAAGGCCACAGTGAAACTCACAGAAGCAACACAGCTGG
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACCACCCGACCCACAGCCAAACCTACCCAGCCTGGAC
CCAGGCCCGGAGGGAATGAGGAAGCAAGAAGAAGGCCTGGGAACATTGTTGGAACCCCTTCCAGGCCCTGTGCG
CCTTTCTCATCAGCTTCTTCCGAGGGTGACAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC
ATCTCTTTTATATTATGCCGCTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGGAAAAGAAACCTTCTTTCTGGAGTTTGCAGAGTTTCAG
CAATATGATAGGGAACAGGTGCTGATGGGCCCCAAGAGTGACAAGCATACACAATACTTATTATCTGTAGAAGTT
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTTCATGAATTTCCAGTGTTTCAGTAAAT
AGCAGCTATGTGTGTGCAAAATAAAAGAATGATTTTCAGAAAAA

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FIGURE 210

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKFVPCLLLVTLSCILGQAPRQKQGSGTGEFFHFQTGGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEEAKKAWEHWCWKPFQALCAFLISFFRG

Important features:**Signal peptide:**

Amino acids: 1-19

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

DNA photolyases class 1 proteins:

Amino acids: 58-69

Tyrosine kinase phosphorylation site:

Amino acids: 64-71

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids: 4-15

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FIGURE 211

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCGGGTCCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCGAGCCAAGTGGAGCCAGAACCGGACCCCGTGCGCC
GGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGGTGTCACTCCTGGTGCAAGAAGGTACGCGCTCTCAGACATG
CTCCTGCCGCTGGATGGGGAACCTGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTG
GACTGTGGCGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGGCCTGCCGCCACGACGACGTCTTCTTTC
CGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCGAGCATCTCGGCTCTGG
GCCGACGTTACGCGCGACGAGGACCTGGCTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGC
CGGGCGCGCTTGAGCGTGGGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC
CGTGGATCTGCGCGGCCCTGCTCCAGCCCT

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FIGURE 212

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603
<subunit 1 of 1, 197 aa, 1 stop
<MW: 20832, pI: 8.74, NX(S/T): 2
MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPDGLVSLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTCGAL
GTRHLASSSWTPSACPAATTTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR

Important features:**Signal peptide:**

Amino acids 1-19

N-glycosylation site:

Amino acids 35-39

Glycosaminoglycan attachment site:

Amino acids 81-85

N-myristoylation sites:

Amino acids 82-88;118-124;153-159

C-type lectin domain proteins:

Amino acids 108-118

FIGURE 213

[illegible]

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FIGURE 214

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCIIQSLALTWYSLSFIPFARDAVKKCFVCLA

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FIGURE 215

GGATTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGGGGAGGCCCAGGACAGGCCCCACCC
TGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCCTTGCCCTGGG
TCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAACCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG
AAAAGGCAGTCACCCGCGAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC
AGCCACCACCCACACAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCCCTGCCCTGGCCCCG
CACCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTTGAGCTCCACAGGTTTCAGGTATCATCA
TCTGCTTGGTGGTTCTGGATGCCCTCCTGGTCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACA
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT
TTAAATTATTTGTCTTCCGCCTGAGTTCCTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGGTGGTCT
CATTATCCTGGACATTGTCTCCTGTTCAGGAGCACCAGTTTGAGGCTCTGGGCTGCTGATTCTGCTCCGGC
TGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTGAGAACGGCAACTCTTAAGGT
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACT
GATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTA
CTCTCACACAGCCACCGTGAAAGTCCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTCAATCACAGAGAAACAAACCAAAATCTATAAAGATATTCTGAAAATATGACAGAA
TTTGACAAATAAAAGCATAAACGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 216

MATWDEKAVTRRAKVAPAERMSKFLRHFTTVVGDDYHAWNINYKKWENEEEEEEQPPPTPVSGEEGRAAAPDVA
PAPGPAPRAPLDFRGMLRKLFSHRFQVIIICLVVLDALLVLAELLDLKIIQPDKNNYAAMVFHYMSITILVFF
MMEIIFKLFVFRLLSFTSLRSWMPVVVVVSFILDIVLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSE
RQLRLRKQMNVLAAKIQHLEFSCSEKPLD

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FIGURE 217

GGGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT
ATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC
TGCACCTTTTGAACCTGACATCAAACCTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTC
CATGAGTTCAAAGAAGGCCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTC
TGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAAATAATGTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAATAATTCTGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTGGGGAGTGAGAGGACAGGATAGTGCAATGTTCTTTG
TCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCA
CATCTTATATTCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT
TATAAATAAACTGAGCACCTTCTTTTAAACAA
AAAAAAA

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FIGURE 218

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

FIGURE 219

[illegible]

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FIGURE 220

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYILMPFLLNQCGSLLYYTL
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISP EWVRTRPFPILP
FPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 221

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA
ATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACTTTGCCAGTGGGAAGTACCTAGTGAAA
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTC
CAGCACCAATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCGT
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCTGCTGAAGAACAACCTTTCATTTTGTAAAGCCA
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGC
AGAGTGCCCTGCTTGTTATGAATCTAATGGAACTTCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGACA
GTGTGTCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACGT
CAGTAACGCCACCTGTCTAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCATCTTTCGAAAGTTTGAGTG
TGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCCACAACGTGGGGCTCCAAAGCTTCCCTCTA
CCTCTTGGCCCTTGCCAGCCTCCTTCTCGGGGACTGCTGCCCTTGAGGTCCTGGGGCTGCACTTTGCCCAGCACC
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTTCCTGCTCTGCCCCGTTTAA
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGG
TTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASSECPSHANTSCISSASSSLET
PVRLYQNMFCSAENCS
EETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGT
SCRGKPKWCYEEEQCV
FLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTS
APTTSNVGSKASLYLL
ALASLLLRGLLP

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FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCCTCAC
TGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCGGCGCGCTGCTGTGGGTCTGTGCTGCTG
AATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC
TTTGGGGGCCCCATGACCCGCAGCTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA
GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCCACG
GTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAT
GCCGGAAGGATAGCACACGAGAGAGCTTCCAGTGCGACTCCCAATACAGCGGGGAGTTCCAGCACGAGGTTT
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGAC
CTGCCAGGCTCGCAGGCCACCCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCCTCA
CCCACAGCCATGCCATCTCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG
TCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCTTCGAGTTGGGGCGCTGAGC
CAGCTCCGCACGGAGCACAAAGCCTTGCACTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTC
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGG
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTCAGTGTTTACAGAGATGCAACCAATAGACAGAAAC
CAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCTTTCAATCCTAGCAC
CCACTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAAACAA

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FIGURE 224

MVPAAGALLWVLLLNLPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD
RLAGPAAAEELLAATVSTGFSRSSAINNEEDGSSEEGVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWPPSPPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGK
LHGLSGRLRVGALSQLRTEHKPCTYQQPCPNRLREECPLDTSLCDTNCSQSTTSTRTTTFFPTIHLRSSPSL
PPASPCPALAFWKVRIGLEDIWNLSLSSVFTEMQPIDRNQR

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FIGURE 225

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGGCCGGCCTGGCGGGCGCGGTTGGTCCTGCTAGCTGGGGCAG
CGGCGCTGGCGAGCGGGCTCCCAGGGCGACCGTGAGCCGGTGACCGCGACTGCGTACTGCAGTGCGAAGAGCAGA
ACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC
GGGACGACTGTAAGTATGAGTGATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCTCAGT
TCCATGGCAAGTGGCCCTTCTCCGCTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCTCAATG
GCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCCATGTACCACACCTGTG
TGGCCTTCGCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG
AGAAAATGGACTACTTCTGTGCCTCCACTGTCTATCCTACACTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC
TGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCTCCTACCTGA
GCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTGGTGTGGTGGC
TGGCCTGGTGCCTGTGGAACAGCGGGGCTGCCTCACGTGCGCAAGTGCGTGGTGGTGGTCTTGCTGCTGCAGG
GGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCATCTGGCACATCA
GCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTCTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG
ACAAGTTCAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCCGCCCTGCTGGCCTC
CCTTCTCCCCCTCAACCCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGAAGGATGTGGGCCCG
AATCATGTGGCCAGCCACCCCTGTTGGCCCTCACAGCCTTGGAGTCTGTTCTAGGGAAGGCCTCCAGCATC
TGGGACTCGAGAGTGGGCAGCCCTCTACCTCTGGAGCTGAACCTGGGTGGAACCTGAGTGTGTTCTTAGCTCTA
CCGGGAGGACAGCTGCCTGTTTCTCCCCACAGCCTCCTCCCCACATCCCCAGCTGCCTGGCTGGGTCTGAAG
CCCTCTGTCTACCTGGGAGACCAGGGACACAGGCCTTAGGGATACAGGGGGTCCCCTTCTGTTACCAACCCCCA
CCCTCCTCCAGGACACCACTAGGTGGTGCTGGATGCTTGTCTTTGGCCAGCCAAGTTTACGGCGATTCTCCCC
ATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACCGTTGCCCTAGCCAGGTTCCCA
GGAGGCCTCACCATACTCCCTTTAGGGCCAGGGCTCCAGCAAGCCAGGGCAAGGATCCTGTGCTGCTGTCTGG
TTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGGTGACAGGGCCGTGAGCATGGGCC
TGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGTGCGGGGAAGAGGTGTGGCTTCAAAG
TGTGTGTGTGACAGGGGGTGGGTGTGTTAGCGTGGGTAGGGGAACGTGTGTGCGCGTGTGGTGGGCATGTGAGA
TGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTACCATCAATAAT
CACTTGTGGAGCGCCAGCTCTGCCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT
GTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCCTCCTGCAAACCTCACAGGGTCCCCACACAACAGTGCCC
TCCAGAAGCAGCCCCCTCGGAGGCAGAGGAAGGAAATGGGGATGGCTGGGGCTCTCTCCATCCTCCTTTTCTCCT
TGCCTTCGCATGGCTGGCCTTCCCTCCAAAACCTCCATTCCCCTGCTGCCAGCCCCTTTGCCATAGCCTGATTT
TGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCCAG
AGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAAGGTGACCC
CTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT
CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTCTGTGCCCTGACCCCTTGTCCCTCTTTGAGGGA
GGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTGGCCTGCGCTAGCTTCTTTGATACTGAAAACCTTTT
AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCCAAGCCTCAAAAAAAAAAAAAAAAAA

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FIGURE 226

MAGLAARLVLLAGAAALASGSQGDREPVRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV
TVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPASSPMYHTCVAFWVSINAW
FWSTVFHTRDPTDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLLMLTVHVSYLSLIREFDYGYNL
VANVAIGLVNVVWWLAWCLWNQRRLPHVRKCVVVVLLQGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSS
FLEDDSLYLLKESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

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FIGURE 227

TTCCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCCCTTCCCCGGGGTCTC
TGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGCGTTGCCACCCACGCGGACTCCCCAGCTGGCGCGCCCC
TCCCATTGCTGTCTGGTTCAGGCCCCACCCCCCTTCCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCG
GCTGCACTTTTCGTCGCGTTTCGGCCCCGGCCTTCGCGCTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTA
TCATCCTGGTTCGAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCC
ATGTGACCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCCTTCTAC
AGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAAGGGTTAGCATCGCTGAGTGAGGACG
GAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCT
CTGTTATCAATATTTTGGCTGATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCC
TGACTTCAGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTG
AGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACC
CCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTG
GAGGGTCCCTCCGAAGTATTCAGCGCAGCCTCTGTGTAAAGACTGACTACCTGGACTGATCGCTGACAGATCC
CACCTGCCTGTCCACTGCCCATGACTGAGCCCAGCCCCAGCCCGGTCCATTGCCACATTCCTGTCTCCTTCT
CGTCGGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAG
CAGCCTGGGTTTCAGCCAGTCAGTGACTGGTGGGTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCTTGT
TGTGTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCACCTGCCCAAGACTCACCTCCCTTCCCCTCTGCAGG
CCGACGGCAGGAGGACAGTCGGGTGATGGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACTTAGG
GGGGACCCCTGGGCCTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCA
GGTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGC
TCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTCAGGCCTGAGGGGGAACCATTTTTGG
TGTGATAAATACCCTAACTGCCTTTTTTCTTTTTTGGAGTGGGGGGAGGGAGGAGGTATATTGGAACCTTCT
AACCTCCTTGGGCTATATTTTTCTCTCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTCTCCTTGG
TCCCAGACCTTGGGGGAAAGGAAGGAAGTGCATGTTTGGGAACGGCATTACTGGAACATAATGGTTTTTAACCTCC
TTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGCCACTCCAGAGCTGCA
GTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGG
TGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATC
AAGGTGATTGTGATTTTGAATAAAAAAAGAAATTTGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 228

MGAAVFFGCTFVAFGPFAFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIH
GDSPYYFLTSAFLTAIIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSLLCKD

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FIGURE 229

CGGGAGGCTGGGTGCTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG
GCCGACCCCGCGCAACATGCAGCCACGGGCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGCTC
TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAG
CCCTCTCCACGCTGGGCTCCCCCAGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCA
CTACGCCAGGCACCCCCAAAACCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG
ACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACCTGCGAAATT
TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT
CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCT
CCTACTCTGAACCTCGAGCTTGTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCG
TGNAGGGTGCTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA
CACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACACCACATGTACACCAACGTCA
GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTGTCTCTATG
CATCGGACACCTTGATAAGAAGGGTCCTGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG
CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTG
CACTGTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA
GGGCAGTCATTGGATCTGAGTTTATCGGGATTGGTGGAATTATGACGGGACTGGCCGGTTCCCTCAGGGGCTGG
AGGATGTGTCCACATACCCAGTCTCTGATAGAGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTG
TCCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG
TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGG
CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCTCCCCATACCTTG
TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCTTGACACAGTCGGTCCCGCAGA
GGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCTAGTTCAATTCACAAGCATATGCTGAGAATAAACATGTTA
CACATGGAAA

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FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTTPGLTTPGTP
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTC
STPWAESSTKFRHHMYTNVSGLTSTFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNVPPDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDVSTY
PVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYQLSTSCHSHLVPQNGHQATHLEV
TKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359,
357-362, 394-399, 427-432 and 472-477.**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

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FIGURE 231

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG
CCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTCGGCAGGGCCC
GCTTTTTAGAAAGCTTGATTTCCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGG
AACTCGGGGGCGATTGGCTGGGAAGTGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGAC
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAAGTGGAGGCAAGAGG
GTTGCTCAACGCCCCGCCTCATTGGAACCAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT
GATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCTTTCCCCGCCCTTGAGACCCTGCAGCACCA
TCTGTCAATGGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCG
GCCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCGTCCGCTGTGGCGGGAAAGCGGGCCC
CCAGAACCAGACACCCGTGGCAAGAGGACCCAGAACCAGGACGAAAAGTGTATGAGAAGAAGCCAGACTCC
CATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATC
CTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAG
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCAAGATCCAG
CTGCCAGAGGATGAGTGAACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATT
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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FIGURE 232

MAAGLFGLSARRLIAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPEDENLYEKNPDSHG
YDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 233

GCGGCGGCTATGCGGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCCGGCGGCTGGTGCCTTGCAGAACCCCCA
CGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGCTGCCTTCCGGGGACGTAGCCGCCACATTCCAGTTCCGC
ACGCGCTGGGATTCCGAGCTTCAGCGGGAAGGAGTGTCCCATACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTG
ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCAATCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCA
CCCTTCCTGCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAATCT
TGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTC
ACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTC
TCTGTGCTGCTGAAGGCAGATCGCTTGTTCACACACAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGC
AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCACTTGTATTTGATGCCTTCATCAG
GGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGAGCCCTGCCCCCTGGCTTCA
GAGAGCCGAGTCTATGTGGACATCACACCTACAACCAGGACAACGAGACATTAGAGGTGCACCCACCCCGACC
ACTACATATCAGGACGTATCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC
AACAACTCTCGAAACCTCAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCCCAGTGCCCTTC
CTGCATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAACACCCAC
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCCCTCACC
ATCACCTCCAAGGGCAAGGAGAAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC
CTCCTGGAGATGCTGATTCACTGCTGCGGCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTG
AAGTGGACCGAGTACACGCCAGATCCTAACCATGGCTTCTATGTGAGCCCATCTGCTCAGCGCCCTTGTGCC
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCAGTCTCTGATGGC
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC
AACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGTGCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTC
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCC
CCTCTGATTCTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTTTC
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTGAGGGCTACAGCTGTGTGT
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTAACCTAGAAATTCATTTCCCTCACCTGTAGT
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAGTGGTGGTGGCTGCTGTATTGGACAGCACAGAAAAGAT
TTCCATCACACAGAAAGTCCGGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT
GTAGTGGATGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTCCGTGGAAAAA

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FIGURE 234

MPLALLVLLLLGPGGWCLAEPDRSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHYRLFPPKALGQLISK
YSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDKSWKELSNVLSGIFCASLNFIDSTNTVTPT
ASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA
RCTSISWELRQTL SVVFD AFITGQGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTY
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTHPYR
AFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT
EYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLLVLNLTPTDFSMYPYNI
CLTCTVVAVCYGSFYNNLTTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

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FIGURE 235

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAGCACCAGGAGC
CCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGTGGGCTACCCCTGGTGGTGG
TTATGGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG
GATGTTCCCTCTGGAACCTCCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCC
AAGTTCTACGGTGCCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCTCCCAATGTGGATCCTGAGGCCA
CTCCTGGTTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA
CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG
CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCCTCTCCAGCAGTATGACCG
GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAATGGGCTACAACCTGAGCCCCA
GTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCA
GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT
CAGCTTCGAGGACTTCGTCAACATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCAC
CAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCAATAGTGAGG
ACCGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGC
AGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC
TGATGCCAGTGGTGAAGTGTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAAC
GAGCCCATTTTCTCCAAAGTGGAACTCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT
GCCACACCCATAAATCCTTGTTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG
GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCTCAGT
CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTCATTTTTTTTCAATTTGGGGCCAAAAG
TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

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FIGURE 236

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG
TPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSHSGYISMKEKQALVNCNWSS
FNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL
VSRYPERSANPAMQLDRFIQVCTQLQLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 237

[illegible]

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FIGURE 238

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV
PLKLSVPPSDGFPFAGGSAYQWPPSWGLPAMDSWPPEDPWQMMAAAAEDRLGEALPEELSYLSSAAALAPGSGP
LPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRPWSLIHRVLPDHPWGTLPNPSVSWGGGGPGT
GWGTRMPHPHEGIWGINNQPPGTSGWGNINRYPGGSWGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGV
LRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-
274, 270-275, 280-285, 281-286, 305-310

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FIGURE 239

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCCG
CTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCCGGAGAGCTCAAGCGCCC
AGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCCT
GGGTGGTGTCAATCCCCTTGGGGCTGCTGTTCTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCT
CTTAGAGGAGCTGCTCAGCAAATACCAGCACAAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
GGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGCCTGGGGCCACCAGCCTGCTCTGTTCCCCAG
CCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTG
TTCTGTTTTGTTTGTGTTTGTGTTTGTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCA
TGCCCTGAAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACATACAGGCATGC
ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA
CTCCTAGGCTCAAGCAATCCTCCTGCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCACCCCTGCTGCG
CTCTGGCTCTGTTCTTAACATTCTGCCAAAACAACACAGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCCTTC
ATGTCACCTCTTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCC
AGGGCTGGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTCCTTAGCCCCG
TGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCCTCGCGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA
AGGGCCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGGCTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGA
AGACAGCCAAGGTCAACCCCTCCCGGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGTGCTACTTGAC
CCCAAGCTCCAGTGTGGAACCTCCTTCTGGCTGGTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAG
GGTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTTTTTAAACAAACC
CACGTCCCAGCCTGGGTAACATGGTAAGCCCCGTCTCTACAAAAAATCCAAGTTAGCCGGGCATGGTGGTGCG
CACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGC
TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGAC
CCTGTCTCAAAAA

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FIGURE 240

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS
NMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGRGGSRLCSVLFVCFETGSHSATDAGVQ
WHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

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FIGURE 241

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC
CTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG
GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT
CTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCA
TTGAAGCCTGTGTCCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAG
CAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTGCGTATGCTG

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FIGURE 242

MSGGLPLVLLLTLLGSSHGTGPGMTLQKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTLHHARSQHHVCNT

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FIGURE 243

GGCAAGTGGAACTGCTGGCTTGGTGGATTTGCTAGATTTTCTGATTTTAACTCCTGAAAAATATCCCAGAT
AACTGT**CATGA**AGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT
CATCAACAAAGTGCCCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTTCCCTTTATGGATCC
ATTAAAGCTTCTTCTGAAAACTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAAATGA
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGT**TGA**CATCAAGATAA
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT
CAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAGCAATGAATACATTA

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FIGURE 244

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855  
<subunit 1 of 1, 93 aa, 1 stop  
<MW: 10161, pI: 7.39, NX(S/T): 0  
MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLKTLGISV  
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV
```

Important features:

Signal peptide:

Amino acids 1-18

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FIGURE 245

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT
GCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT
CGGGTGTGTGCTGGTGCCCCAGCTGAAGCCAACAAGAGTTCTGAAGATATCCGGTGCAAAATGCATCTGTCCACC
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGA
GCCCATGCCAGTGCCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC
CACCACCATCAAGGTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCTTCCTGAT
GCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCCCTGGAGCGTGTGGAAGGTGC
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGAT
GGGCTGGTGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGGCTACTT
CTCCCTTCCTCGGTTCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCTCCTTCTCCCTAACTTTAGAAATG
TTGACTTTGGCTATTTTGTATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTT
GAAGGGAGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTC
TCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTC
TTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTGAGCATGTGTTCCCTTCTGCAGTGGTTCTTATC
ACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC
TGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCAGTGAAGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCA
CTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTC
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA
ACACCACAGCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACTTCGTTGTACCACTGCATGGAGAGAAAAATTTG
TCCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTGTTTTATTTCTCTCA

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FIGURE 246

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS**Important features:****Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

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FIGURE 247

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAAAGCTTTCTGAGTTTCAAAAACAACAGA
CTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT
TTCTGATGTGGGGTTCCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTG
AAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAG
TTCCCCCTCCCCCTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTGTAT
GATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTTTTTCTTGGCACTAAT
CAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTAGTAAATAGAAACCTGTGTTTATTCTCAG
GTATTTTAGAAACAACAGCCATCATTTTATTTTATGTGTGTGTTCTTGGCTGTATTCATAAATTATATTTTGG
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCA
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTATCTTCA
GATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

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FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECIVDLCLLRICYKLSGVPNQCRVPLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 249

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCAGCCCAAGTGAGGGGCCCCGTGTTGGGGTCCCTCCC
TCCCTTTGCATTCCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGGCCGCGTTGATG
CGGAGCAAGGATTTCGTCTGCTGCTGCTTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGATGACGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCAGTT
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTCCAGCGT
TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG
TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
CATGGTGGAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCAAA
AAAGGGAGAAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTTCCATTATG
CAACTTGTCTATGTAAATAATGTACACATTTGTGAAAATGCTATTATTAAGAGAACACACAGTGGAAATT
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATACTCCTAGAATAACTTGTTA
TACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAACATGGAGCATTTGTTAATTTACACAGAAAAT
TACCTTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
TTCCAAATAATGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAAACAAACAG
CCACAAATACCTTTTTCAAAATTTTAGTTTACCTGTAATTAATAAGAACTGATACAAGACAAAACAGTTCC
TTCAGATTTACGGAATGACAGTATATCTCTCTTATCCTATGTGATTCCTGCTCTGAATGCATTATATTTTCCA
AACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAATTTTACAGATGGCAAAAAATTTAA
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTTATTTCTTAAAGATTGGCCATAACCTATATTTT
GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGTCTG
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCGGTACTATCCTCAAATTATTTATTTTATAG
TGCTGAGATCCTCAAATAATCTCAATTTTCAGGAGGTTTACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACTCTGCAGCATCTG
CTTTATTTGCAAAAGGGCTAGTTTTCGGTTTCTGTCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTGAAACCACTTTACTACTTTTTTTAACTT
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCTGACTTTAACTTTTG
TAGACCACAATTCACTTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
AGATTGAGTTTGAGCCTGTATATCTATTAATAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA
CATTTTCTGCACAGGTCTGCAAAAACAAAATTATAAACTAGTCCATCCAAGAACCAGTTTGTATAAACAGGT
TGCTATAAGCTTGTGAAATGAAATGGAACATTTCAATCAACATTTCTATATAACAATTATTATTTTACAAT
TTGGTTTCTGCAATATTTTCTTATGTCCACCCTTTTAAAAATTATTTTGAAGTAATTTATTTACAGGAAATG
TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
TTTGTAATTTAGGAAAAATGTATAATAAGATAAATCTATTAAATTTTCTCCTCTAAAACTGAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 250

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCRDMCCPSTRCNNGICIPVTESILTPHIPALDGTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

Signal peptide:
amino acids 1-25

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FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTGGGATTAC
AGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATTTCTTCAAATTCATGGCAAATATTTCC
CTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAAT
ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTAGATTATAGGTTTTAACATACTTGTG
AAAATACTTGAATGTGTTTTAAAGCCTTGGGCAGAAATTCGTATTGTTGAGGATTTGTTCTTTTTATCCCCCTTT
AAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCAACCAAAAAATGGCAAACATCACCAGCTCCCAGAT
TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA
CCCTACAACCTACTACTTCTTGGGACCTCAAGCCCCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAA
ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGT
TCCTCCTCCTGGTTTGGAGTCCTTTCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC
TGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA
ACACATCAAACCTTGCTAAGCGGCGGATACCCCGAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC
AGCAGATGTCACAGGATTAAATGTGCAGTTTGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTGAATTTGG
ATCAGCTCCAAGCAGTGAAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTAAAGTGAGCCTTTGAA
TACATCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCAATTACCTCCTGCAGTCTGAC
AAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACCAGAGTTCTGTGCATAACAGGAT
CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG
TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTGTGCATGGCTGGTGCCAACCAAACAGAGGAAGAG
GATAGCTCACGTGATGTGGAAAACACCAGTTGGTCAATGGCTCATTCTGTTAAAAAGCAGCCCTTTTGCTTTTTTG
TTTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGTGGTGGTCTCATA
TTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG
GTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCCAAAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACC
ACCCTGGGCAACATGGTGAAACTCTGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGCGCGTGCC
TGTAATCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT
CTGAAAAGA

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FIGURE 252

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPPPGLESFPSQAKLRESTPGDSPSTVNK
LLQLPSTTIENISVSVHQFQPKHIKLAARRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP
SSENSNQIPISLYSKSLSEPLNTLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQ
SPVSSSESAPGTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPKQKRIAHVMWKTVPVQWLIR

Signal peptide:
amino acids 1-24

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FIGURE 253

GGGCGCCCCGCTACTACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTCGCAGATGTGGAGCTCAT
GGGGCTGTGGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGCGGTAGCGCGGGGTGGCTGCGCGCGGG
GGAGGAGAGGAGCGGCCGGCCGCTGCCAAAAGCAAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAA
GCAGAAACAATATCAGCGGATTTCGGAAGGAGAAGCCTCAACAACAACCACTTCACCCACCGCCTCCTGGCTGCAGC
TCTGAAGAGCCACAGCGGGAACATATCTTGATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGCAGA
TGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCAGCAGCATGAGAGCCAACGTGGA
GCTGGACCACGCCACCCTGGTGGCTTCAGCCCTGACTGCAGAGCCTTCATCGTCTGGCTGGCCAACGGGGACAC
CCTCCGTGTCTTCAAGATGACCAAGCGGGAGGATGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAA
AAAGCACAAAGCGCCTGTCTCGACATTGGCATTGGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACAC
CACTGTCTCTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACACACACGC
TGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGAAGGTTTGGGAAGTCTGCTT
TGGAAGAAGGGGGAGTTCCAGGAGGTGGTGGCAGCCTTCGAACATAAGGGCCACTCCGCGGCTGTGCACTCGTT
TGCTTTCTCCAACGACTCACGGAGGATGGCTTCTGTCTCCAAGGATGGTACATGGAAACTGTGGGACACAGATGT
GGAATACAAGAAGAAGCAGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGGCGGGTCCGCGCCGTG
CCGCTGGCCCTCTCCCCAACGCCCAGGTCTTGGCCTTGCCAGTGGCAGTAGTATTCATCTCTACAATACCCG
GCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCAACTTGTCTTTGACATCACTGG
CCGCTTTCTGGCTCCTGTGGGGACCGGGCGGTGCGGCTGTTTCAACAACCTCCTGGCCACCGAGCCATGGTGGGA
GGAGATGCAGGGCCACCTGAAGCGGGCCTCCAACGAGAGCACCAGCCAGAGGCTGCAGCAGCAGCTGACCCAGGC
CCAAGAGACCTGAAGAGCCTGGGTGCCCTGAAGAAGTGACTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGA
GGGATCTGGCCTCCTCATGGCACTGCTGCCATCTTCCCTCCAGGTGGAAGCCTTTCAGAAGGAGTCTCCTGGTT
TTCTTACTGGTGGCCCTGCTTCTTCCCATTGAACTACTCTTGTCTACTTAGGTCTCTCTCTTCTTGGTGGCTGT
GACTCCTCCCTGACTAGTGGCCAAGTGCTTTTCTTCTCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGC
ACTGAGGAGAATGGTAGAGAGGAGAGGAGAGAGAGAGAATGTGATTTTTGGCCTTGTGGCAGCACATCCTCAC
ACCCAAAGAAGTTTGTAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGATG
GGAGACTGGGATAGCTTCCCATCACAGAACTGTGTTCCATCAAAAAGACACTAAGGGATTTCCTTCTGGGCTCA
GTTCTATTTGTAAGATGGAGAATAATCCTCTGTGAACTCCTTGCAAAGATGATATGAGGCTAAGAGAATATCA
AGTCCCCAGTCTGGAAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTGATGAAAGTGGTAAAAGTGGGAA
CCAGTGTGCTTTGAAACCAATTAGAAACACATTCCTTGGGAAGGCAAAGTTTTCTGGGACTTGATCATACATTT
TATATGTTGGGACTTCTCTCTTCGGGAGATGATATCTTGTGTTAAGGAGACCTCTTTTCAAGTTCATCAAGTTCAT
CAGATATTTGAGTGCCCACTCTGTGCCCAAATAATATGAGCTGGGGATTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 254

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQKQYQIRIRKEKPQQH
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFSPDCRA
FIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSDITVLIWSLKGQVLSTI
NTNQMNNTAAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGE
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQLQQQLTQAQETLKSGLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

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FIGURE 255

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGCCAGGTGCCCC
GTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGGAGAAGCCCCCTTCCTCGGCGCTGCCAACCC
GCCACCCAGCCCATGGGCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGG
GGCCGAGCCTGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC
CTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGGCCAGT
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGCTGCAGGGCTGCCTG
CCCATCTAGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCT
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGA
GGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 256

MANPGLGILLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFSLLAALLLAVG
LALLVRKLRKQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 257

[illegible]

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FIGURE 258

MGLFRGFVFLLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTTASTYLFEATEKRFFFKN
VSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLLLGGKKQNEYGPPG
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF
FPDKVQTEKASIMFMQSIDSVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLL
KISQRIVCLVLDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL
PTYPLGGTSICSGIKYAFQVIGELHSQLDGEVLLLTGDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS
KITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNS
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM
NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYS
LKVRAHGGANTARLKLRLPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFVVSQVPSLPLP
DQYPPSQITDLDATVHEDKIILTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKES
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL
VLSVIGSVVIVNFILSTTI

Signal peptide:
amino acids 1-21

Putative transmembrane domains:
amino acids 284-300, 617-633

Leucine zipper pattern.
amino acids 469-491, 476-498

N-glycosylation site.
amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,
811-815, 832-836, 837-841, 852-856, 896-900

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FIGURE 259

CGCCGGAGGCAGCGGGCGGTGGCGCAGCGGGCGACATGGCCGTTGTCTCAGAGGACGACTTTTCAGCACAGTTCAA
ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCACTGCTTGAGAAGCTGCTGGACCGCC
CGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCTGTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA
GTCTACTGCCATGGAACCTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAG
CCACCGGGGAGGACCCCTGAGGGCTCAGACATCCTGAACACTTTTGAGAGCTACCTTGCCGTTGCCTCCACCGTGC
CCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTGTCTGGCCTCAC
TGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCAGTGGTGAAGGTGGACACTTCCTCCTGGACCCGTGGTT
TTTTTGCGGTCACCAATTGTCTGCATGGTGATCCTCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA
TGACCGGCTCCTTTCTATGAGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG
TGGCCTCATTGGTGGACTTGGCTGCATCCAGTGTGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGGCCACCA
TCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCTG
TTCTTGCGGCCCATGTGTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCTTCGGTGGCCTCCA
GATTCAATTGATTCCACACACCCCCCTCTCCGCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACT
ACGTCTTCTTCATCACCAGCCTCATCTACCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT
CACTGTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACTTTGCTGACCTATGTGGCCGGC
AGCTCACCGCCTGGATCCAGGTGCCAGGGCCCCAACAGCAAGGCGCTCCCAGGGTTCTGTCTCTCCGGACCTGCC
TCATCCCCCTCTTCGTGCTCTGTAACTACCAGCCCCGCGTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT
ACCCCGCACTCCTCAGCTCCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCTA
AGATTGTGCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGG
GCTCAGCCTGCTCTACCCTCCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTGCTTCAGAGCCTT
TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCCTAAAGTTTCACTTGGGGACAGAGAG
CAGAGCACTCGGGCTCATCCCTCCCAGATGCCAGTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATA
TTCCAGTCATATTAACAGAACTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACA
GCTGATGGTTAACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACAA
GCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCCAGCTGACAGCGAGATGCAA
GCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCCTGGCATGGTCAGTCTCAGGC
CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACTGCCCACTAACCAGACTGGAAAACCCAG
AAAGATGGGCCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCT
GGCCTGGGTTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA
GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCGTATTCAAAAA

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FIGURE 260

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIFFSLGIGSLLPWNFFITAK
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAI FMVIT
ALVKVDTSWTRGFFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRP
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG
VVM SFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,
448-472

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FIGURE 261

CGGACGCGTGGGCTGCTGGTGGGAAGGCCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACACACCTGTTTA
AAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATAAAGGAGGGCAGAAAT
GGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTCCCTT
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGTGTGTTGGGTGCTGGCCTTCTCTGTGGAAGTGTCT
GGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGGAAAACACCACCAAGCAAGTGA
AACACATAATGTGATTGCATCAGACAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCA
CACACAGCTGCATGCCTATATTGGTGTTCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGG
TAACTCCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAATCACCACCACGCTGGG
TCTGTTGTCCATGCTGCAGCTGATGTTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT
AATGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGGAGTGGTTTCCTTCTTGATGCATGCTGG
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCATGGTGCATA
CTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGGCCATGCTTTTCTCTGC
CGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGCACAGCCACAAGCCCGA
TGCCACGGGAGGGAGAGCCCTCAGCCGCTGGAAGTGGCAGCCCTGGTTCTGGGTTCCTCATCCCTCTCATCCT
GTCAGTAGGACACCAGCATTAATGTTCAAGTCCAGCCTTGCTCCAGGGCCCTTGCCATCCAGTGAGAACAGC
CGGCAGGTGACAGCTACTCACTTCTCTCAGTCTCTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCA
GAGGGGAGGTGAGGTAAAACCTGAGTAATGGAAAAGCTTTTAGAGTAGAAAACACATTTACGTTGACGTATGCTA
TAGACATCCCATTGTGTTATCTTTTAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCTATTCTC
AGGGAAGATGGAATTTAGTTTTAAGGAAAAGAGGAGAATTCATACTCACAATGAAATAGTGATTATGAAAATAC
AGTGTCTGTAAATTAAGCTATGTCTCTTTCTCTTAGTTTTAGAGGCTCTGCTACTTTATCCATTGATTTTTAACA
TGGTTCCCACCATGTAAGACTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTCTATAGCACCCTCA
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTC
TCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTTAAACAGCTCCTTTGGCACGTGCCT
CTCTGAATCCAGCCTGCCATTCCATCAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT
TTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAATACCTGTCTCCACATTCCTAGAGAGGAGCCAAAGTTCTAGT
AGTTTCAGTTCTAGGCTTTCCTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAATTT
TAAGTGATTTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAAATGTATGGTTGTCC
TTTTTTTTTGTTTTTTTTTTTTTTAAATATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG
TCAGCTTTGGCGACACTGTGTCTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAAGTGTTCGCT
ATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTTCTTGTCTTTCTTAACCTTTCCCTC
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATTTGTGTGGGATGAATTCCTATCAGGACAA
CCACTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATTTCTTATCCCCCTTCAAAGAAATTACCTTTGTG
TCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAAATTGACACAATCACTAATCTGGTAAT
TTAAACAATTGAGATAGCAAAAGTGTAAACAGACTAGGATAATTTTTTTTTCATATTTGCCAAAATTTTGTAA
ACCCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTACTTTCTATACCATTTCAAAACACA
TTACACTAAGGGGGAACCAAGACTAGTTCTTCAGGGCAGTGGACGTAGTAGTTGTAAACAGTTTCTATGAC
GCATAAGCTAGCATGCCTATGATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTT
GTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT
GCATACAATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACATATATGGTTGCCTAGATTCTCTCTGGAACCTGAC
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

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FIGURE 262

MDDFISISLLSLAMLVGCYVAGIIP LAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQIGNSHVHSTDDPEAARSSNSKITTTL
GLVVHAAADGVALGAAASTSQTSLVLFVVAIMLHKAPAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVT
YLGLSKSSKEALSEVNATGVAMLF SAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI
LSVGHQH

Signal peptide:
amino acids 1-18

Transmembrane domain:
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 263

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGG
GCAGGGGTGACAACAGGTGTCTATCTTTTGTATCTGTGTGTGGCTGCCTTCTATTTCAAGGAAAGAC
GCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCC
AGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCCGCTTAACTTGTGG
TTGGAGGAGAGAACCCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTG
GACCAGAAGAAAGGAAAGGTCCCTCTTGTCTGTGGTGCACATCAGGAAGGCTGTGATGGGAATGAA
GGTGAAAACCTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAAAGTAGAGA
AGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGC
TCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCT
TTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTTCCGCGGGGGCTGCT
TGCCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGCTCCTCTGCTGTGCTATCTCTGTCTGTACATGT
TGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAACAGCCCCACGGGGAAG
GAGGGGTACCAGGCCCTCCTTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGAGCAGCCTGAAGCG
GCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGGAGTGAAGCAGCTCAGGAATGGCGAGTACCAAG
CCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTCTGGCC
TTCCTGCACCTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGGATATGCAGC
AGTGCCTTTTCGATAGCTTTACTCTACAGAAGGTGTACAGCTGGAGACTGGCCTTACCCGCCACCCCG
AGGAGAAGCCCTGTGAGGAAGGACAAGCGGGATGAGTGTGGTGGAGCCATTGAATCAGCCTTGGAGACC
CTGAACAATCCTGCAGAGAACAGCCCCAATCACCCTCCTTACACGGCCTCTGATTTTCATAGAAGGGAT
CTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCACAAACACGAAT
TCAAACGGCTCATCTTATTTTCGACCAATTCAGCCCCATCATGAAAGTGAAAAATGAAAAGCTAACATG
GCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTCGGGCAGTTTCATGCA
GAATTTTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGGAAAG
AAGAAATAAATGAAGTCAAAGGAATACTTGAACACACTTCCAAGCTGCCAATTCAGGAACCTTACC
TTCATCCAGCTGAATGGAGAATTTCTCGGGGAAAGGCACTTGATGTTGGAGCCGCTCTGGAAGGG
AAGCAACGCTCCTTCTCTTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTA
GGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTTCCTTTTCAGTCAGTACAACTCTGGCATA
ATATACGGCCACCATGATGCAGTCCCTCCTTGGAAACAGCAGCTGGTTCATAAAGAAGGAAACTGGATT
TTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTGAGACTTCATCAATATAGGTGGGTTTG
ATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTCCACAGCAACCTC
ATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACTCTGGCATGAGAAGCGCTGCATGGACAGCT
GACCCCGGAGCAGTACAAGATGTGCATGCAGTCAAGGCCATGAACGAGGCATCCACGGCCAGCTGG
GCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAAGCAAGTACAAA
AAAACATGAACCTCCAGAGAAGGATTTGTGGGAGACACTTTTTCTTTCTTTCTTTTGAATGAAAGTG
GCTGCAACAGAGAAAAGACTTCCATAAAGGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAA
AGCCTCCGATTTCTCTCTGTTGGGCTTTTTTACAACAGAAATCAAATCTCCGCTTTGCTGCAAAAGT
AACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAAGATGCTTGTGAGATTATAAGCCTAATGGTG
TGGAGGTTTTGATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATTATG
ATTTAAGAGCAGTTTTGTAATAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAATATCAGAAGGCAGGAGAGGAGATAGGCTTA
TTATGATACTAGTGAGTACATTAAGTAAATATAATGACCAGAAAAGAAAAGAACCATAAATATCG
TGTCATATTTTCCCAAGATTAACCAAAATAATCTGCTTATCTTTTGGTGTGCTTTTAACTGTCT
CCGTTTTTTCTTTATTTAAAAATGCACTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTA
CCACTTTTGAAGCCTTACAAGAGAGCACAAGTTGGCCTACATTTTATATTTTTTAAAGAAGATACCTT
GAGATGCATTATGAGAACTTTCACTTCAAAGCATCAAATGATGCCATATCCAAGGACATGCCAAATG
CTGATTCGTGCAGGCACTGAATGTGAGGCATTGAGACATAGGGAGGGAATGGTTGTACTAATACAGA
CGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATG
ACACTTTCTGCTTTACAGAAAAGGAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAG
AAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAGATATACCGT
GTGAACCAACAATCTCTTTTCAAACAGGGTGTCTCTCCTGGCTTCTGGCTTCCATAAGAAGAAATG
GAGAAAATATATATATATATATATATATTTGTGAAGATCAATCCATCTGCCAGATCTAGTGGGATG
GAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTATTTTTTAAATTAAGC
AGTTCTACTCAATCACCAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAACATTTTTTAA
AATAAATACAGTTAACATAGAGTGGTTTCTTCATTCTGTGAAAATTATTAGCCAGCACCAGATGCAAT
GAGCTAATTATCTCTTGTGCTTCTGCTTCTGTTGCTCAGAGTAACTCATTTGTTTAAAGCTTCAA
GAACATTCAGCTGTTGGTGTGTTAAAAATGCATTGATTGATTGTACTGGTAGTTTATGAAATTT
AATTAACACAGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

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FIGURE 264

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSL
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS
FTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYE
LTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMANLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNT
QPGKKVFYPVLFQYNPGIYYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGED
VHLYRKYLHSNLIVVRTPVRLFLWHEKRCMDLTPQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ
KTSSKKT

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FIGURE 265

GGATGCAGAAAGCCTCAGTGTGCTCTTCCTGGCCTGGGTCTGCTTCCTCTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTTCCTGCTCACCCGTTTGGAGCTACCAACCATAGCAGCTGCCAAGAGCCCCCAGGCCCTGGGTCCC
TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCGATTTTCGCGGGTTGTGTGGTGCTGA
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTCACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCCT
TCCTGGGCAAACCTAAGCTCCTTGACAGGATCCTGGAGATTACGCCCCACCATGCCGGCTCTACCGATCTCAGG
TTGACCCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCACCTGGCTCACTGCCCTACCTTTATTGATGCTG
GTAGTAACCTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA
ATGTGACAGACCTAGACACAGTGGACATGGCATCCTGGACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCCTGAAATGGCCA
AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGGAGTCTCAGCTGCTCTCTTTT
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCCTGCCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
GGGGTGGAGACTCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCATCTCAATGCTCAGCAGGTGT
CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGGCCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTTCCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATCTGCCCCTTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC
TCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTCTTCTAGGGGCTGTGCTGAGCTGAGCTCATTCTCCCTT
TTCTGTGAAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCCCTGTTTCCCATCCCTGGGCCCCGTCC
TGTTACTCCTGCTGTTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTGTAGCTGAGGCCAGGGCCACCCCT
TCCTTTTGGGCTCATTCACTCCTGCTCCTGGTGTGCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAACCCCCACGGCACAATGGTGATATGCCCTGAGGCTTG
GAATTGGGTGCTTTTATGTACAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAAGAATTTATGGTATGGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTAGCTGCCGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTTGGGTACTGCTGCTACTGGGCATTGGCGTGGGGG
CAGATGAGGCTCCCCCGCTCTCCGGTCTGCTGCTCTGGGCGATCCATGGTGTGCTGGGCTGTAGCAGGGC
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGCTGTAAGGCTGGGCGAGGCGCTCCAA
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
TCTACCGACACATGCAGGAGGAGTTCGGGGGCGGTTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCTG
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCACTTCTGCTGT
TGCATGCGGAGCGCATCAGCCTTGTGTTCCTGCTTCTGTTTCTGCAGAGCTTCTTCTCCTACATCTGCTTGTG
CTGGGATACCCGTCAACACCCCTGGTCTTTTACTGTGCCATGGCAGGCACTCTCGGCTTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC
CAGAGGGTCTAGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCCCTCCACCTCCTCT
TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTCCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCACTGATGGAGATGCGGCTCCGGG
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCTCAAGTACCTCTTTATCCTTGGTATTTCAGATTC
TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAAGTGTTCGCCCTAAGTTTCATAT
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCGCTGACATCTAGGACTTCATTATTCTATAATTCAGGACCACAGTGGAGTA
TGATCCCTAACTCCTGATTTGGATGCATCTGAGGGACAAGGGGGGGCTCTCCGAAGTGAATAAAATAGGCCGG
GCGTGGTGACTTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTTAAAAAAGTGAATAAAATGATAATAT

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FIGURE 266

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACWMASRFSRVVLVLI
DALRFDAQFPQSHVPREPPVSLPFLGKLSLQRIEIQPHHARLYRSQVDPPTTMRQLKALTGSLPTTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLFPGAFSKAFFPFSFNVRLDTVDNGILEHLYPTMDSGEWD
VLIAHFLGVDHCGHKHGHHPHMAKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFL
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAAQASALHLNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAETLPTVIAELQQFLRGARAMCIESWARFSLVR
MAGGTALLAASCFCILLASQWAI SPGFPFCPLLLTPVWGLVGAIAAYAGLLGTIELKLDLVLLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPPIPGPVLLLLLFLAVFFSDSFVVAEARATPFLGSGFILLVVLHWEQQLLPKLL
TMPRLGTSATNPPRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVA
ALVALLAAVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMLPRAVAGL
AASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGLERTKSQGPLTVAA
YQLGSVYSAMVTALTLLAFPLLLLHAERISLVFLLLFQSFLLLHLLAAGIPVTTPGPFTVPWQAVSAWALMAT
QTFYSTGHQPVFPAIHWHAAAFVGFPEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLWPFLCESQGLRKROQP
PGNEADARVRPEEEEEPLMEMRLRDAPQHFYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFIF
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034,
1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 267

[illegible]

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FIGURE 268

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTDFDPLPALQPHGYDQPGTE
PLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEATFAELHIVHYDSDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLQGTILFSTEEEPSKLLVQNYRALQPLNQRMVVFASFIQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLNRKSVVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

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FIGURE 269

GTGGCGCTGGCGGTTGCTGTCAGCTGATTCCCGGGGTTGGTGGCAGCGGCGGTAGCAGCAATGGACTTTCTCCTG
GGGAACCCGTTTCTCAGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC
TGCGGGCACCCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCCC
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGCTCAACCTCATCCAGTCCCTGGGCTGACGCGTTCCGCAGC
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCCATGACTGAC
CTGGACATGCTGTCAACCATCCACACACCCAGAGGACCGTGTTCACCTCAGAGACACAATCAGGACAGGATTCTG
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCCCTCTGCCCGCCCCGCCATACTCTCCG
GTGACACGCCCCATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG
TGAGGGTGATGTCCGAGATGCTGACGGAGCTGGTGCCACCCAGGCCGAGCCGCGAGACCTGGAGCTGCTGCAGG
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCCTGAGTGATACCTGCTCCGGGCCCATGCCCCAAGGA
GCCCTTCAGAGCCACACTGCCAGTCCGAGGCCCTGGCTGGAGGCTGGCCACAGTGGAAATTCGCCGAGCCTATTG
TCCCTACCTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG
CCCCCTGAGGAGCTGCGGCGGCCAGGTACGAAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCTTGCCCTCCATCCTTCTCTGT
TCCTTCTGGCCGGGCACACAGCACTGGGGCTCACCTCTTGTTGATCCTCTTGACTGGGAGAGGTGCCTTTTG
TATCCCCAATTAAAGGTAGAAAACC

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FIGURE 270

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGRHFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation site:

Amino acids 41-45

N-myristoylation sites:

Amino acids 6-12;23-29

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FIGURE 271

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCCATGGGGC
TCGGGTTGAGGGGCTGGGGACGTCCCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCGTGAAGCCCCCGCAG
GCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGGTGACCCCCACTCCAGGCCCTACATGGGCATCCGTGCGCT
TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCACTGCTTCAGCC
ACAGAGACCTCCGCACTGGCCTGGTGGTGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCCACCCAGCAGGTGT
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCGGC
TGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCACAG
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG
CCAAGGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGAACCGGG
CTCACGGCTCGTTTCCTTCTCGGGCCTCTGGTGGGCGACCCCAAGACCCCGACGTGTACACGCAGGTGTCCG
CCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCCCAGCCCGGCCCTGCCTGGGACCACCAGGC
CCCCAGGAGAAGCCGCTGAGCCACAACCTTGCGGCATGCAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG
TGGCTGGGCCCCACGGGAAGCCTGATGTTGAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA
TGCAAAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAGAAA

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FIGURE 272

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAVLSTAEPTQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRLPGRRAP
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCR
NRAHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

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FIGURE 273

GAAGTTCGCGAGCGCTGGCTATGGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG
GAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCCG
AGCGCCCGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCT
ACGACAAGGTACTTTCTTTGTCATGAGGATTCAACAACCCCTGTGGCTAACCCCTGTGCTTGCAATTTACTCTCATCA
AACGCCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG
GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTTTCAGAGAGTCACTGGCTCTGCCATCACTG
ACCTGTACAGCCCCAAACGGCTCTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCCTATGACA
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGA
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAAATGTTT
CGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA
AATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGCTGAGGCTGTCACTCCAGAGGCCCAATATACCCC
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTACAGCCCTGGGTTCCAGCCCACTCTCTACCAGATCCCTA
GCCTCTACTGTTCCCTATGAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACC
TGGAGCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAACTTGCAGAAC
CATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAGCAGTTACAAGTGGAGTACCGCATCAGCAAAGTGCCT
GGCTGAAGGACACTGTTGACCCAAACTGGTGACCTCAACCACCGCATTGCTGCCCTCAGAGGCCCTTGATGTCC
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG
CTACGTCACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT
TTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTGTCTGCTGGTGGGAG
ATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGGACAGGAATCCGCAGACCCTGCAGCTCCAGCCCTGAAG
ACTGAAGTGTGGCAGAGAGAAGCTGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTA
GGAGAGGAGAAAAGCAGAGCAGCCTCCTGGAAGAAGGCTTGTGAGCTTTGTCTGTGCCTCGCAAATCAGAGGCAA
GGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC
ACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGGAGTTCAGATACTCTCTGTTGGGAACAGG
ACATCTCAACAGTCTCAGGTTGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC
AGCCCAAGCAGGGAGTGTCCCCCTCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTTTTTTAA
GTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTTTAAACACAGTCATTAAAAATGTTTATAAATCAAAA

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FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLLIKRLQSDWRNVVHSLSEASINIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLT
GDDCFQVGKVAYDMGDYYHAIPWLEEAVSLFRGSSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPLQTRDT
YEGLCQTLGSQPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRP
PYAEYLQVVNYGIGGHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGSDTLHAGCPVLVGDKWVANKWIEYQGFEFRPCSS
SPED
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Leucine zipper pattern:

Amino acids 34-56;41-63

Ribonucleotide reductase small subunit signature:

Amino acids 340-356

N-glycosylation sites:

Amino acids 242-246;482-486

Cell attachment sequence:

Amino acids 27-30

Tyrosine kinase phosphorylation site:

Amino acids 189-198

N-myristoylation sites:Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;
457-463;473-479

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FIGURE 275

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATCAAGCCCTG
CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAACTGTGTCTGTTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATAC
ATATGCGAGTTCACCATCCCTAAATAGGTCTTTCTCCAATGTGTCTCCAAGCAAGATTATCATAACTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCTTCTGCGGTATAGGGGATC
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTAGTCTTTC
TCACTTGTAACAAACCCAGTTTGTTTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCT
AGGTGCTATATAATCCAAAACTTTTCAGCCTGTGTCTCATTCTGTCCATGCTGGCAATAATACCTGTGTGAGCC
CATACCCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCTGCCATATCAGAACACAAACCCC
TGAAGAGGTTCTGATTTGATTTTTTTTTTCTTCATGCCTACCCTTTTTTGGAAAGTTTCCAGCCGCAATTTGA
AATGAAATGACAGGTGTATATTTGATCAATTTTCATTCCCACCATTGCATTACAACCTCTAAGCTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTTTCTGATATTTAT
TTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAACTGAATTTAAG
AATGCTATCTTGGAAATTCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGTCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAACTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGAGGGGAAATGGGCTTTTTTAGAAG
CAAACAATTTAAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC
CACTTTGCAAACCTTTAACTACACATGCTTGAATTAAGTTTATAGCTGTTTTTATTGCTCAATAATAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLDQTTSHSRKARKHKKRRVRDKDGD LKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQKWSDEACRSSKRYICEFTIPK

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FIGURE 277

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAGGAAGCCACCAGAC
TCCACGGTGTGGGGCCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCT
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG
CCCTGGTCCCTGTCTGTGGGCATCTATGCAGAGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCCTGG
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC
GTGACAACCTGTACCTTCTCCAAGCATTATGTATCATCCTTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG
TGGTGGCCTTGACCTTCCGGAACCGACCATTTGACTTCCCTGAACGACAACATTGGAAGAGGAATTGAGAACTACT
ATGATGATCTGGACTTCAAAAACATCATGGACTTTGTTTCAAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACC
GAGATTGGAGCAAGAATCAGTACCAGGACTGCAGTCCCCCTGGACCCCTGGCCTGTGGGGTGCCTTACACCTGCT
GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATCGACAAGGAGCGTTTCAGTGTGC
AGGATGTATCTACGTGCGGGGCTGCACCAACGCGGTGATCATCTGGTTTATGGACAACCTACACCATCATGGCGT
GCATCCTCCTGGGCATCCTGCTTCCCCAGTTCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGG
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCA
CGGGATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACACTCAGTACTGACCAAAGCCAGG
GCTGTGTGTGCTGTGTAGGTCCCACGGCCTCTGCCTCCCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGC
TTTCCCCGAGGCAGCTCTGGAATCTGTGCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGG
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCCATTTTATCTCTGGCAGTGCCTTGGCGGTGGTATTCA
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGGCATCTGGGGAA
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCCAGGTGCCTT
GAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTAGTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTT
GTACAGATAACAGGAGTTTCTGACTAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTGCCCTTCCCCAAC
CAGTTTGTAAATCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

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FIGURE 278

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIIYAEVERQKYKTLES AFLAPAILILLGVVMFM
VSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQTIDFLNDNIRRG IENYYDDLDFKNIMDFVQK
KFKCCGGEDYRDWSKNQYHDCSAPGPIACGVPTCCIRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:
amino acids 1-44

Transmembrane domains:
amino acids 22-42, 57-85, 93-116, 230-257

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FIGURE 279

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACACCTGGGAAGAT
GGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAAGCCACCCCTCAGTCCCAC
TGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT
GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCAACAGCTAACATCCTCCAGCTGCAGGTGAAGCC
CTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTTGGTCAA
GACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCAC
CCGCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCT
GGTGAACGCCCTTAGCTAAGCAGGTCAAGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTG
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAG
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAA
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGA
CAACATCCCGTTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCTGTTGGACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGA
CCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTT
CACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAA
CATCAGCTCTGATCGGATCCAGCTGATGAAGTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCAGTGTCAATTGGT
GAAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTG
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAAAAA

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FIGURE 280

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILOQLPLLSAMREKPAGGIPVLGS
LVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGENTPLVKTIVEFHMTEAQATIRMDTSASGP
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYPAIKGDITQLYLGAKLLDSQGVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPE
EFMVLLDSVLPESAHLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL
FTLGIEASSEAQFYTKGDQLILNLNLISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSL
VKALGFEEAESSLTkdALVLTPASLWKPPSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

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FIGURE 281

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCGCGTTCT
CTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCTGCCACCGCTGCTTCCCTGGC
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTGATCTGTGGCCCTGTGCCCTCCGTGTC
CTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGTTCCCGAGGT
GAGGGTCTCTCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCTGGACTCCCACGCTCGAGCCCCGCCAGA
CATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT
GATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCA
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG
GGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT
CCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTG
CCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC
TGGGAGAAAGAGAGGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG
CGGGAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCTGCATCCTATG
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTACCCCGAGAA
AGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAG
GTGTCCCAAGGCACCGGGCCGGGTCTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGC
CCTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCA
GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC
AAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCCTAG
CCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCA
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAA
AAAAAA

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FIGURE 282

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTEPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFP SRLPNQCVLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

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FIGURE 283

CGGATGGTGCGCCCGGTGGCGGTGGCGGCGGCTTGGCGGAGGCTTCCTTGGTGGGATTGCAACGAGGAGAAGAT
GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG
GCCTCGCCCTGTTGTGCTGCGCCGCGCCGCGCCGCGCTCGCCTCAGCCGCCCTCGGCGGGGAATGTACCCGGTG
GCGGCGGGGCGCGGGGACAGGTGGACGCGTCCGCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTA
GGGCGACGGCTCCACAGGCCCAGGCCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTGCGA
CTTCTCCAGCCAGTCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCCACACCTTTTCAGGCGC
CGCTCGGCCCCCTCGCGACCAACCCCTCCGGCGGCGGAACGCACTTCGACCACCTCTCAGGCGCGGACCAGACCCG
CGCCGACCAACCCCTTTCGACGACCACTGGCCCCGCGCGCCGACCAACCCCTGTAGCGACCAACCGTACCGGCGCCACGA
CTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGG
CCCCCTCTTCGCTCCTCCAGAGTATGTATGTAACGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC
AGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAGAGGGGCTTTTACC
TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGAACAGGT
AAGCAACAGAGGGTGGAACTGAAGTTTATTTTATTTTATTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCA
TACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAATATTTTATATACCTTTATTCTCTTACTTTAT
ATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAGAGTCGCCAA
TTTTTCTCTGGGATAATTTCTGTAAATTTTATGGGAAAAAATTATTGAAGAATAAATCTGCTTTCTGGAAGGGCT
TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATACCATTGGAGTTTGAGGAAAT
TTGTTGTTGGTTTATTTTCTCTCTAATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG
GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGGAGACCAAAA
GTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGAATAATGTACTGT
TATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTTATCTTTGACCTTATGTGAGGCACTTGGCTTTTTGTG
GACCCCAAGTCAAAAACTGAAGAGACAGTATTAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAAACC
TGGGTATAACCAAGATCTGCTGCCACTTACGAGCTGTGTTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGT
TTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAATT
CTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGAACTTTTAGCTCCTTG
ACAAAGAAGTGCTTTTATACCTTAGCACTAAATATTTTAAATGCTTTATAAATGATATTATACTGTTATGGAATAT
TGTATCATATTGTAGTTTATTTAAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCGTGAATCCTAGCACTTT
GGGAGGCCAAGGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCT
CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG
AGAGGGGAGACTCTGTCTTAAAAA

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FIGURE 284

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAA AVASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATAPTAQAPRTGPPRA
TVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTFPAAERTSTTSQAPTRPAPTTLSTTGPAPTTPV
ATTVPAPTTPTPTPDLPSSSNSSVLPTPPATEAPSSPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHC
ETCKEGFYLNYSGLCQPCDCSPHGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 285

AACACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCTGCTCTGGGG
AGGGAGAGGGCGGAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCGGTGACGGTGCAGGAAGGCCTGTGT
GTCCATGTGCCCTGCTCCTCTCCTCCTACCCCTCGCATGGCTGGATTACCTTGCCCGCAGTAGTTCTATGGCTACTGG
TTCGGGAGAGGGCCAATACAGACGAGTAGCTCCAGTGGCCACAACAACCAGCTCGGGCAGTGTGGGAGGAG
ACTCGGGACCGATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGAAGA
AGTGATGCGGGGAGATACTTCTTTCTGATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACC GGCTCTCT
GTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCCTGGAGTCCGGCTGCCCCAGAAT
CTGACCTGCTCTGTGCCCTGGCCCTGTGACGAGGGGACACCCCTATGATCTCCTGGATAGGACCTCCGTGTCC
CCCTTGGACCCCTCAACCACCCGCTCTCGGTGCTCACCTCATCCCACGCCCCAGGACCATGCAACAGCCTC
ACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCAGAACAGACCGTCCATCTCAACGTGTCTCTACCCGCT
CAGAACTTGACCATGACTGTCTTCAAGGAGACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA
TCCCAGAGGGCCAGTCTCTCGCCCTGGTCTGTGCACTGATGCACTTGACAGCAATCCCCCTGCCAGGCTGAGC
CTGAGCTGGAGAGGCTGACCTGTGCCCTCACAGCCTCAAACCCGGGGTGCTGGAGCTGCCCTGGGTGCAC
CTGAGGATGCACTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGTCTCAGCAGGTCTACTGAACGTCTCC
CTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGGAGCTGGAGCCACAGCCCTGGTCTTCTG
TCCTTCTCGCTCATCTCTCGTTGTAGTGAGTCTCTGCAGGAAGAAATCGGCAAGGCCAGCAGCGGGCGTGGGAGAT
ACGGGCATAGAGGATGCAAACGCTGTACGGGGTTCAGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAGAC
AGTCCCCAGACAGCCTCCCCAGCTTCTGCCCGTCTCTAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC
AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGCACCGAGTACTCGGAGATCAAGATC
CACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCAGAGGC
TGATTCTTGTAGAAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAAGC
ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTATTTTTTAACTAAAG
ACAGACAAATTCCTA

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FIGURE 286

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREGANTDQDAPVA
TNNPARAVWEETDRDRFLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNILI
PGTLESGCPQNLTCVVPWACEQGTTPPMISWIGTSVSPDPSTTRSSVLTLPQPDHGTSLTCQVTFFGASVTTN
KTVHLNVSYPQNLMTVVFQGDGTVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS
NPGVLELPWVHLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK
KSARPAAGVGDGTGIEDANAVRGSASQGPLEPWAEDSPPDQPPPASARSSVGEGLQYASLSFQMVKPWDSRGQE
ATDTEYSEIKIHR

Signal peptide:
amino acids 1-15

Transmembrane domain:
amino acids 351-370

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FIGURE 287

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCAGAGGCGGGACTGTCGTCTGGGGGAGCGCGCCAGGAGGCTCCTCAG
GCCGACCCAGACCCCTGGCTGGCCAGGATGAAGTATCTCCGGCACCGCGCGCCCAATGCCACCCCTATTCTGGCC
ATCGGCGCTTTACCCCTCCTCCTTTCAGTCTGTAGTGTACCACCCACCTGCAAGGTCCAGGAGCAGCCACCG
GCGATCCCCGAGGCCCTGGCCTGGCCCACTCCACCCACCGCGCCAGCCCGGCCCCGTGCCATGCCAACACCTCT
ATGGTCACCCACCCGGACTTCGCCACGCAGCCGCAGCACGTTCAGAACTTCCTCCTGTACAGACACTGCCGCCAC
TTTCCCTGCTGCAGGACGTGCCCCCTCTAAGTGCGCAGCCGGTCTTCCTGCTGCTGGTGATCAAGTCCTCC
CCTAGCAACTATGTGCGCCGCGAGCTGCTGCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG
CGCCTCCTCTTCTGGTGGGCACAGCCTCCAACCCGCACAGGCCCCGCAAGGTCAACCGGTGCTGGAGCTGGAG
GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCTG
TTCTTACAGTGGCAGGAGACAAGGTGCGCCAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC
ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCTGGCCGCCACCTCTTCGTGGGGCAACTGATCCAAAAC
GTGGGCCCCATCCGGGCTTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAATGAGCGGTACCCACCC
TATTGTGGGGGTGGTGGCTTCTTGTCTGTCCGCTTACGGCCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGGAC
ATCTTCCCATTTGATGATGTCTTCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCACAGCGGC
ATCCGCAGTCTGGCGTGGGGCTCCATCGCAACACCTGTCTCTTTGACCCCTGCTTCTACCGAGACCTGCTG
CTGGTGCACCGCTTCTTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACCCAGCCCACTCACCTGCGGC
AATCAGACACAGATCTACTGAGTCAAGTCAAGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGCGAC
ACCTTCTCTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAAGTTTGGAGTTTGATGA
GTGAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT
GGCTGGAGGAACCTCCAGAAAATATCCATCTTCTTTTGTGGCTGCTAATGGCAGAAGTGCTGTGCTAGAGTTCC
AACTGTGGATGCATCCGTCCCGTTTGAGTCAAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA
AGCAGTGCACCTGCAGTGGTTAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAACTCCTGTGTC
CACATAGAGCTGACGTGAGAAATATCTTTCAGCCCAGGAGAGAGGGGTCTGATCTTAACCTTTCTGGGTCTC
AGACAACCTCAGAAGGTGGGGGGATACCAGAGAGGTGGTGGATAGGACCGCCCCCTCCTTACTTGTGGGATCAA
ATGCTGTAATGGTGGAGGTGTGGGCAGAGGAGGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG
GGTCTCATTAGGAGCCCCCATCCCTGTGTTCCCCAAGAATTAGAGAACAGCACTGGGGCTGGAATGATCTTT
AATGGGCCCCAAGGCCAACAGGCATATGCCTCACTACTGCCTGGAGAAGGGAGAGATTAGGTCTCCAGCAGCCT
CCCTACCCAGTATGTTTACAGATTACGGGGGACCGGTGAGCCAGTGACCCCTGCAGCCCCCAGCTTCAGG
CCTCAGTGTCTGCCAGTCAAGCTTACAGGCATTGTGATGGGGCAGCCTTGGGGAATATAAAATTTTGTGAAGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

<subunit 1 of 1, 372 aa, 1 stop

<MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRHRRPNATLILAIGAFTLLLFSLVSPPTCKVQEQQPAIPEALAWPTPPTRPAPAPCHANTSMVTHPDFAT
QPQHVQNFLLYRHCRRHFLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGREKVRGLQLRLLFLVGTA
SNPHEARKVNRLLLELEAQTHGDILQWDFHDSFFNLTLKQVLFLOWQETRCANASFVLNGDDDVFAHTDNMVFYLO
DHDPRHLFVQGQLIQNVGPIRAFWSKYVPEVVTQNERYPYCGGGFLLSRFTAAALRRAHVLDIFPIDDVFL
GMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPFCFYRDLLLVRFLPYEMLLMWDALNQPNLTGNTQIY

Important features:**Type II transmembrane domain:**

Amino acids 15-34

N-glycosylation sites:

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

TonB-dependent receptor proteins signature 1:

Amino acids 1-32

N-myristoylation sites:

Amino acids 308-314;316-322

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FIGURE 289A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGCGAGGCGAGCCTCCTCCAGGAGCGGGGCCCT
GCACACCAATGGCCCCCGGGTGGGCAGGGGTGGGCGCCGCCGTGCGCGCCCGCTGGCGCTGGCCTTGGCGCTGGC
GAGCGTCCTGAGTGGGCCTCCAGCCGTGCGCTGCCCCACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCA
CGGGCTGGGCCTCCGCGCGGTTCTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT
CACCAGGATCACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAGGTGAG
CGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCTGCAAGT
CCTTCCAGAATTGCTTTTCCAGAGCAGCGCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCCAGGGGAT
CCCGAGGAAGGCGTTCCGCGGCATCACCGATGTGAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGA
AGATGGAGCCTTCCGAGCGCTGCGCGATTTGGAGATCCTTACCCTCAACAACAACACATCAGTCGCATCCTGGT
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTGCCACCT
GGCCTGGCTCTCGGATTGGCTGCGACAGCGACGACAGTGGCCAGTTACACTCTGCATGGCTCCTGTGCATTT
GAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTGTGCCCAGCCCCCACTCGGAGCCCCCATCTTG
CAATGCCAACTCCATCTCCTGCCCTTCCGCTGACGCTGACGAATAACATCGTGGACTGTGAGGAAAGGGCTT
GATGGAGATTCTGCCAACTTGCCGGAGGGCATCGTCGAAATACGCTAGAACAGAACTCCATCAAAGCCATCCC
TGCAAGAGCCTTCAACCACTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC
AGATGCCCTTCCAGGGCTGAAATCACTCACATCGCTGGTCTGCTATGGGAACAAGATCACCGAGATTGCCAAGGG
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAACTGCCTGCGGGTGAACAC
GTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT
CGCCCTCTGCACTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT
GGCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCGCGCGGACTCGCCAACAA
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTGAGCAGCGA
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCACGATTGTGGACTGCTCAACCAGAAGCT
GGTCCGCATCCCAGCCACCTCCCTGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGA
GGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG
AGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCTGGAGACCGTGCACGG
GCGCTGTTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACCTGATCAGCTGTGTGAGTAATGA
CACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC
CTTCACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG
GCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTAGGTGCCAGAAGCCATTTTCTCAAGGA
GATTCACATCCAGGATGTGGCCATCCAGGACTTACCTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC
GCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGC
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACAT
GTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAACGGGCTGCG
GTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTTGAAGGCTCCTTCAACGACCTCACATC
TCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAA
GGCGGGGTACAAGGAGCCTGGCATCGCCCGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC
CCCAACCCACCGCTTCCAGTGCAAGGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAG
CCCGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

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FIGURE 289B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCTGTGAGCATGGAGGCACC
TGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG
ATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG
TGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTC
TGTCAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAG
CTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTGCGTGGACACAATCAAT
GGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCTTCTGTGAACACCCCCACCCATGGTCCCTACTGCAG
ACCAGCCCATGCGACCACTACGAGTGCCAGAACGGGGCCAGTGCCATCGTGGTGCAGCAGGAGCCCACTGCCGC
TGCCCCACAGGCTTCGCCGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG
GAACTGGCCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC
CTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGC
CTGAGTTCCCCCTCAACACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTG
ACGCTAAACCAGACCTGAACCTAGTAGTGGACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCA
GCAGTGGGCATCAACAGCCCCCTCTACCTTGGAGGCATCCCCACCTCCACGGCCTCTCCGCCCTGCGCCAGGGC
ACGGACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG
GCCCTCCCACCAAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCCCTGCACCGTGTGCAAGCACGGCCTGTGCCGC
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAGGCTGGACCGGCCACTCTGCGACCAAGGAGGCCCGG
GACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC
GAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCAT
GGGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA
CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA
GCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGCTGTGGGCCCCAGTGCTGCCAGCCCACCCGACGAAGCGG
CGGAAATACGTCTCCAGTGACGACGAGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGC GGCTGC
CTCGCGTGTTCCTAAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT
GTGGGACCCCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTA
TATTGTAAATAAACAATAAATAGAACTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 290

MAPGWAGVGA AVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITR
ITKMDFAGLKNLRVLHLEDNQSVIERGAFQDLKQLERLRNKNKLQVLPPELLFQSTPKLTRLDLSENQIQGIPR
KA FRGITDVKNLQLDNNHISCIEDGA FRALRDLEILTLNNNNISRI LVT SFNHMPKIRTLRLHSNHL YCDCHLAW
LSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME
IPANLPEGIVEIRLEQNSIKAIPAGAFQYKKLRIDISKNOISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHLAQNPFFVCDCHLKWLD
YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLVR
IPSHLPEYVTDRLNDNEVSVEATGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG
KWLRKRRI VSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLRALPRGM
PKDVT ELYLEGNHLTAVPRELSALRH LTLIDLSNNSISMLTNYTFSNM SHLSTLILSYNRLR CIPVHAFNGLRSL
RVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTPT
HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGK DCTVPINTCIQNPCQHGGTCHLSDS
HKDGFSCSCPLGFEGQRC E INPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVP E LNL CQHEAK
CIPLDKGFSC E CVPGYSKLCETDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPMVLLQTS PCDQ
YECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELVTLNQTINLVVDKGT PKSLGKLQKQPAVGINS
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHIS
DQGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQ
CTDGSSFVEEVERHLECGCLACS

Signal peptide:
amino acids 1-27

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FIGURE 291

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTTCGCGAGACTCAACTGAGA
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG
CGGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAATCTACACTCGTTGCAAACCTGGCAA
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATG
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA
GCTTCGCGTGGTGCAGACGCGGAAGCTGAAGGAGAACCACTGCCATGTCGCCTGCTCAGCCTTGATCACTG
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTAAAGAGACACAAGGAATGAACATTTGGCAAGGCT
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAGGCTGTGAGGTTTCCTAAACTGGAACTGGAC
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCASTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCT
CCCAATATTCTTCTCAAACCTTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCATTTAAATGTC

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FIGURE 292

MKAAGILTLLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF
QINSAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

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FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCACCAGAGGA
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTAC
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGT
GGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC
TGGGCCAACTACAACACCTTTGGATCTGCAGAGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGAC
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTG
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA
GTGAAATATGGAGAAGGAAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC
CAGAAAACAGCATCTTATTACTCACCCATATGGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTT
AATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACCTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTCAGAGTTT
TGTGGGAGGGAAACCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGA
ATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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FIGURE 294

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG
GGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSP
YGQREFTAGFVQFRVFNNERAAALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS
REITEAAVLLFYR

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FIGURE 295

CAGGCCATTTGCATCCCACTGTCCTTGTTGTCGGAGCCAGGCCACACCGTCCTCAGCAGTGTGTCATGTGTTAAAAA
CGCCAAGCTGAATATATCATGCCCCCTATTAAACTTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTCAAG
CTTTTTACCTTGGTGTCTGCCTGTATCCCACTGTTTCAAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT
CACTTCCCAGATCTGCTTCTCACCAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAACA
TTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTCTGCTGCTCTCCATCAACAGATACGAAAGGAAG
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAAGATTGACATCCCAAGATTGGGAGAGGGTT
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCCCTCCTC
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG
CAGTGCCCACTCATTGCTGTTAATTCGGGTGGACCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGT
GAGCCTGACCCGGTGCATTTCTCAGAAGCAATAGAAAAGTTCATCCGTGAACCTTCTTAAAGCCACCATGGGC
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACC
AAACTGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAAATGTCAATTTTATGGATTGTAGACCCAGTTTTGA
AACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA
CTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT
TGCCAGTGTTAAGTTACAAATGTGGTGTCAATCCATGTTCAAGCAGAGTATTTTAAATTATATTTCTCGGGATTAT
TGCTCTTCTGTCTATAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCA
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAATCCACCGAAGTGT
TCACTGTCTCTGTTAGGGAATTTTGTGTTGTCCTGTCTTGGCTGGATCCATAGCGAGAGTGTCTGTATTTTT
TTTAAGATAATTTGTATTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAA

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FIGURE 296

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFDPDLLLTKRDSFLKRLYRAPIDWIEEYTTG
MADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPKGKKFLLLSINRYERKKNLTLA
LEALVQLRGRITSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCV
LYTPSNEHFGIVPLEAMYMQCPVIAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRAR
VKEKFSPEAFTEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

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FIGURE 297

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTTCGCCGTTACCTTC
TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATCCAGGGATTACT
CCAACGAAGAAAAAGATGGTAATCTTCCAGATATTGTGAATAGTGGAAGTTTCATGAGTTCCTGGTTAATTTG
CATGAGAGATATGGGCCTGTGGTCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTA
CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTATCAA
TCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGTGACTGATTCTCTGAAG
AGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATAAATGGCTCTCTACCCAGAGACCCAGCAC
GTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCTATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAA
GATGATCAGGAAGTCATTCGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT
GGGTCACCTTGATAAAAACATGACTCGGAAAAAACAATATGAAGAAGCCCTCATGCAACTGGAGTCTGTTTTAAGG
AACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTCCTTAGTACAAGGGAACCTT
AATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGGCCAGTTGCATAATAACTGCAAAATTGTGTACC
TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAA
AATGGTCCTGTTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTTCAACT
GCCAACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATTCCTAGAGAG
ACCTTCGCTCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA
GATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG
TTGAGGTTTGATATATGGTGACCACAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG
GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA
TATTAAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACATTTAAAAAAATCTATGTTG
AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

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FIGURE 298

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR
RLVVS LGTV DVLKQHINPNKTS DPFETMLKSLRYQSGGGSVSENHMRKKLYENGVTDSLKS NFALL LKLSEELL
DKWLSYPETQHVP L SQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGT VWSEIGKGF LDGSLDKNMTRKKQYE
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEE VQK
KLYEEINQVFGNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVLQDP
NTWPSPHKFDPDRFDDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS
REEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

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FIGURE 299

CTAGATTTGTGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGACCGCCGCCCTT
GTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT
CGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTA
TGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCTCTGTCAACCCTGGGCCTCTTGCAGTGGAGCTGGCCGSTTT
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC
CCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCC
AGCTGTCACTGAAATGGCTTTATTTCGTCAACGTCTTTGGGCTGAAAAAGAAACCCTTCTGCATTACCTTCATGACG
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTT
TTCCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT
GTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAACTTATATACAGTTTTAGGGGACAATTAAA
AAAAAAAAA

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FIGURE 300

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 301

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGCTGCTGC
TTCGTGTTCTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCCTCCCGGCTCAGAGGAC
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC
CGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCC
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA
GAACGGGGCCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA
GCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG
GTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATCTGGGTGACCCCGGGGCAGGC
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG
GTTGGGCCTCAGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAG
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTTCTTGCCATCCTGAGGAAAGATA
GCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG
GAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTTGTC
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT
CCAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA
CCCATCCTTAAGCTAAGACAGGACGATTGTGCTCCTCCACACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCC
TCACCTGTCAGACCGGGTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC
CGGGCCGAGAGCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGA
AACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

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FIGURE 302

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAF
YSTDYRLVQKVC PDYNYHSDTPYYPG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

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FIGURE 303

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTTCTGGTTGGTGTCTCTACTGA
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA
TCTTTGGAGCGTTTGTCTGTCTATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCA
GTGAAGGTTTGAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT
GGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC
TGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCTCA
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA
ACTTTCTTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA
GAGGAAGCACAACTGTGCCTTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 304

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIHG
DSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSCLKLCLLCQDKNFFLYNQSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 305

[illegible]

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FIGURE 306

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFVFTQLGAQGTLISSEE
LPQIFTSLSIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 307

CCGCGGGACATGAGGTTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCCAAGAAAAATTTTTTGGG
GGGACCAAGTTTGGAGGATTAATGTGAGAAATGGAGACGAGATCAGCAAATTGAGTCAACTAGTGAATTCAAACA
ACTTGAAGCTCAATTTCTGGAATCTCCTCCTCCTTCAATCGGCTGTGATGTCTGGTCCCATCTGTGAGTC
TGCAGGCATTTAAATCCTTCTGAGATCCCAGGGCTTAGAGTACGCGATGACAATTAGGACCTGCGAGGCCCTTT
TAGACATGAAGATGATGAATGCACAACATGAAGGCCAAGAACGGAGCAGTAATAACTCAACTCAGGGGCTT
ACCATTTCCCTGGAAGCTATTTACCACGAGATGGACAACATTTGCCGAGACTTTCTGACCTGGCGAGGAGGGTGA
AGATTGGACATTCGTTTAAAAACCGGCCGATGTATGTACTGAAGTTCAGCACTGGGAAAGGCGTGAGGCGGCCGG
CCGTTTGGCTGAATGCAGGCATCCATTCCCGAGAGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGA
TTGTATCTGATTACAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAAATGGATATTTTCTTGTGTGCCTGTGG
CCAATCTGTATGATATGTGTATCTCAAATCAAACCGATTATGGAGGAAGACGGGTCCCGAAATCTGGAA
GCTCCTGTATGGTGTCTGACCAAAATAGAAACTGGAACCTAGTTTTCGAGGAAGGGAGCCAGGCACACCCTT
GCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGGAGGTGAAATCAGTGGTAGATTTTCATCCAAAAAC
ATGGGAATTTCAAGGGCTTCATCGACCTGCACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCA
AAAAGGCCCCAGATGCCGAGGAACCTCGACAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGGCTTCTGTGTGCGGCA
CTGAGTACCAAGATGGGTCCCACTGCACCACTGTCTATCCAGTACGCGGAGCAGCATCGACTGGGCGTATGACA
ACGGCATCAAATTTGCATTCAATTTAGTTGAGATACCGGGACGTATGGCTTCTCTGCCAGCTAACCCAGA
TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGACAACCTCTACTAGG
CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTT
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAG
TCGTGTCTCTGGCGGTGTCCCTGCAAGAATCTGGTTCTGCCAGCCTGCTCAATTTTGGTCTGTGTTTTTGATG
AGCCTTTTGTCTGTTTTCTCTTCCACCTGCTGGCTGGGCGGCTGCATCAGCATCACCCCTTCTGGGTGGCAT
GTCTCTCTACCTCATTTTTAGAACCAAGAACATCTGAGATGATTCTCTACCTCATCCACATCTAGCCAAAGC
CAGTGACCTTGCTCTGGTGGCACTGTGGGAGACACCACTTGCTTTAGGTGGGTCTCAAAGATGATGTAGAATTT
CCTTTAATTTCTCGCAGTCTTCTTGAAAAATATTTTCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAGGT
CTCTCCCTCCCTCCTCTCTGTTTTTTTTTTTTTTTTTTGAGACAGAGTTTTGCTCTTGTTGCCAGGCTGGAGTGTGA
TGGCTCGATCTTGGCTCACCACAACCTCTGCCCTCTGGGTTCAAGCAATTTCTCTGCCCTCAGCCTCTTGAGTAGC
TTGGTTTATAGGCGCATGCCACCATGCCCTGGCTAATTTTGTGTTTTTGTAGTAGAGCAGGGTTTCCATGTTGGT
CAGGCTGGTCTCAAACCTCCCAACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATACAGGTGTG
AGCCACTGTGCCGGGGCCCGTCCCTCCTTTTTTAGGCCGTAATACAAAGTAGAAGATCACTTTCCTTCACTGTGC
TGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTCCCTTTGTTATTCAGTGTGACCAGGATGGCGGGAGGG
GATCTGTGTGCTAGTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTGCAGGATGGTGAAAT
ATCCCCACTGTGCTCTAATGGGCTTACCTCCTTTGCTTTTGAATCACTTCAAAGATCTAGGCCCTCATCTTAC
AGGTCTTAAATCACTCATCTGGCCTGGATAATCTCACTGCCCTGGACATTTCCCAATTTGTGCTGTGGTGTATCCT
GTGTTTCTTGTCTGTTTTGT
TTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCTGCCCTTGTGTTTCATTTACCT
CAGCACGTACCATCTGTCTCTTTTGTGTTGTTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG
TCTTAACCTCCTGCCCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCATGTGAAAAA
AAAAAAAAAAAA

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FIGURE 308

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPV DVLVPSVSLQA
FKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGOERSNNFNYGAYHSLEAIYHEMDNIAADFPDLARRVKIG
HSFENRPMYVLKFSTGKGVRP VAVWL NAGIHSREWISQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANP
DGYVYTQTQNRLWRKTRSRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVD F IQKHGN
FKGFIDLHSYSQLLMPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI
KFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRONLY

Signal peptide:
amino acids 1-16

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FIGURE 309

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCAGCCTGAGTCCAAGAT
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTCTTCACTTCAAGTCCC
CTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC
AACAAATTCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGTTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG
GGTCAGCATAGTCACCAACTCTGAGTTCCATACAACTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCCAG
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGG
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG
CACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAC
CAATTCTGAGTCCAGCACACCTCCAGTGGGGCCACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG
GGCCAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACTCCAGTGGGGCTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGAGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG
GATCAGCACAGTCCCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCACACAGCCACCAACTCTGGGTCCAG
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACCTCCCATAGTGCATCTACTGCAGT
GAGTGAGGCAAGCCTGGTGGGTCCCTGGTGGCTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGC
CGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT
CTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAACCTGGTTCTGGAGGAGACCAATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC
CTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCCTTT
CATTTCATCCCAGGAGACCCCTCCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCCTCACCTTTCT
TGCTTTTACCAGACACTGGAAGAGATACTATATTGCTCATTTFAGCTAAGAAATAAATACATCTCATCTAACAC
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAC
CTCCATGCTGGACTCCATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 310

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATIS
GSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS
LVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP
HRPRWSPNWFWRPVSIIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCGCGGTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA
GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGAGCCCGGACTCGTCTGCCGCCGCCGTCTGTCGCCGTCTG
TGCCGGCCCCCGCTCCCGCGCGCGAGCGGGAGGAGCGCGCCACCTCGCGCCCGAGCCGCCGTAGCGCGCGC
CGGGCATGGTCCCTCTTAAAGCGCAGGCGCGGCGCGGCGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGGG
CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGCGCGGGCGCGCGCGCGGCGCTGCCGGCCGGGCGCTCG
CGCGCGCTAGGGCGGGCTGGCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTCGCGCGCGCGCG
GGCGGGCGGCGGGCCCGCGGGCGGAGCGGCGCGGGCATGGCGCGCGCGGCGCGCGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCTGGGCTTCTGTCTGGCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
GCCCAGGCGCCGCGCCAGCCCCGAGGGCTGCCGCTCCGGGCAGGCGCGGCTTCCGAGCGCGGGCGCGCG
CGCATGCGCGCGGGGCGAGCTTGCGGCCCGCTCGGACCCAGATGGCGGCCCGCGCGAGCAAGCACTTTCTC
TCGTGGGAGTCATAGCCGCCAGAAATACCTGCAGACTCGGCCGTGGCGCCTACAGAACATGTTCCAAGACAA
TTCTTGGGAAAGTTCAGTTCCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCTTCATGATGCTCAAGTACATGCACGACCACTACTTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
TGAACAGCAGCGAGCCCTCTTTCTTGGGCAAGCAGGCTGGGCACCAGGGAAGAAATGGGAAAACTGGCCCTGG
AGCTTGAGAGAACTTCTGCATGGGGGGCTGGCGTGATCATGAGCCGGAGTGCTTCGGAGAAATGGTGCCG
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGTGGGAAGTGTGTCCGGAGGTTTG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAAATTACCAAGCTATCACATTACACCCCAACAAAACCCACCTACCAAGT
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAATACAGTCCACCGCGAAA
TTGCTCTGATGAGCAAAATACGCAACACAGAAATCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
TGAGTTTTCAGCCCCGCCAGCAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAATACTGTGATTTCGGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGGACGACATTGTATGCAGGTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAAGCAGAAAGGGAAGAAA
TGACGGTCCCTGTGAGGAGGCACGCGATTTACAGCAGACTTTACAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
TGAGTGCACAAAGAGTTGGCCAGAGAAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAACTCCCTGAAGA
AGCTCGTCCCCTTTAGCTCCCTGGGTGCAAGAGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA
TTCCTTTGTCTGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATTCTGACTCAACCCCTGACAAGGCCAACAAGTTGAAGTATGATGA
GAGATTACCGCATTAAGTACCCCTAAAGCCGACATGCAGATTTTGCTGTGTGTGGAGAGTTTCAAGAGCCCTGG
CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTTCTTCTGCGAGCTGCAGCTCGTGTTTACTA
CAGAATTCCCTCAGCGATGTGCGAGCAATACAGTTCTGGGCAACAATAATATTTTCCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCAGTGACAACCATTTTGCTTTACTCAGAAAACCTGGCTTCT
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCGAGTGGGTGGCTTTGATGTTTCCA
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAAGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGAGTAGTCCAGTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCAAACAGTACAAATGT
GCTTGGGGTCCAAGCATCGACCTATGGGTCCACCCAGCAGTGGCTGAGATGTGGTGGAAAAAATGATCCAA
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
TAATTATCTAATTTATTTTTCAAATAATTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
AAGTGGTTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTTGCCTTTGAA
CATCTTTCTTGTGAACATTATGTAGCAGACCTGTAACTTTGACTTGAATGTACCTGATGAACAAAACCTTT
TTTAAAAAATGTTTTCTTTTGAGACCTTTTGCTCCAGTCTTATGGCAGAAAACGTGAACATTCTGCAAGATAT
TATTGTAACAAAACACTGTAAGTCTGGTAAATGTTCTGTTGTGATTGTTAAACATTCCACAGATTCTACCTTTTGT
GTTTTGTTTTTTTTTTTTTACAATTGTTTTAAAGCCATTTATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC
CAGCTAGGTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGAGACGGAGTCTACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGCTCACTTTAACTCCACTTCCCTGTTTCAAGCAATTTCCCTGCCTTTGCTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTTTGATTTTTTAGTAGAGACGGGGTTTACCCT
GCAAGCCAGCTGGCCAGTAGGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
TGGTAGTTTCATTTCGGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGCATTCTCTCTTCTTGACCTT
CTCTTTAAAGGGTAAAAATTAATGTTTGAAGTATGACAAAGATGAATATTACAAATAAATCTGATGTACACAGACT
GAAACATACACACATACACCTTAATCAAAACGTTGGGGAAAAATGATTTGGTTTTGTTCTCTTTCATCTGTCTG
TGTTATGTGGGTGGAGATGTTTTTCATCTTTTACTACTGTTTTGTTTTATCCTTTGTATCGAAATACCTTTAA

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FIGURE 311B

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCCTTTGGAAACGCTTTTTCCCCTCC
TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAATAAACCAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTGTCTCATT
ATTCCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAACTTAAACACGAAAAA

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FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEGS
TSVPIPVVPLRGVDDSYPPQKKSEFMMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLRSLN
SSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYTTTHED
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREEILEWEEF
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNSLKKLVPPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC
DVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGDIVRVGGFDVSIQGWGLEVDVLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:
amino acids 1-23

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FIGURE 313

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCGCGACGGAGGTTGTGACCCC
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACA
GGTGGGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA
ACAAATGGATGATGTGATATATGCAATCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT
TTGGAATCATGGTGTGATGGAAAGGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT
TTGGAAGCATTTTTCATGCTGAGTCCCTTTTACCTTTGATGTTTGTAAACCCATCTTGGTATC
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA
TGTTTGGTGTAAGTGATTATAAAGTGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCAATTA
TCATGAACCATCGGACAAGAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCT
ACCTCAGATTGGAGAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTGTTGGTGGG
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATCCCAGAAG
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA
GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAAACATTCCTC
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCAGGGAAATCCACTTTCACGTCCACCGGT
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG
AAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAGGGGAGAAGAATTTTATTTTACCGGAC
AGAGTGTCATTCCACCTTGCAAGTCTGAACTCAGGGTCTTGTGGTCAAATTGCTCTCTATAC
TGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTAAAGT
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA
TCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG
AGTAAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT
TCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT
TAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAAATCTCTGAA
TGTAATTTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA
TTATTAAACAATCATCAGGCTTTTAAA

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FIGURE 314

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSIFML
SPFLPLMFVNPSWYRWNNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR
MDWMFLWNCMLRYSYLRLKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYF
CDIHEPLQLLIFPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLD
AVHDITVAYPHNIPQSEKHLLOGDFPREIHFHVHRYPIDTLPTSKEQLQWCHKRWEEKEERL
RSFYQGEKNFYFTGQSVIPPCKSELRVLVKLLSILYWTLESPAMCLLIYLYSLVKWYFIITI
VIFVLQERIFGGLEIIELACYRLLHKQPHLNSKKNE

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

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FIGURE 315

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA
CCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACAGG
AATATCCATGGCTTTTTGTGCTCATTGTTGTTCTCAGTTTTCTACGAGCTGGTGTGAGGACAGTG
GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG
CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTCTTCAGGAATCAGTTCCA
TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG
AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAA
CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCTCAGTTCCCAGATTTACGATGAGGA
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCATCGTGGGATA
TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAA
GTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG
CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTCCAT
CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA
GCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT
TGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGGAACACGCACTGGAGGTGACTCT
GGATCCAGAGACGGCTCACCCGAAGCTCTGAGAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
GGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT
GGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG
GTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTACATTCAATCCCCATTTTATCAG
CCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCTGGACTATGAGGGTGGGACCAT
CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGG
CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCAT
ATGTCCAGTGTCTGCGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC
CAGACACAGCCAAGGGAGAGTGTCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAGCCTGCGC
ACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA
GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC
ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAATCCATC
CAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTGCTAGTCACGGACAGT
GATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTTTGA
GGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTTT
GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC
CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCTACTGATTCTATAAGCCCAG
CATTACCTGATACCAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCA
TATCCCTCATTAACACAGACACAAAATTTCTAAATAAAATTTTAACAAATTAACCTAAACAAT
ATATTTAAAGATGATATATACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAA
TATTTAAATATCAACCAGTGAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAA
AAAAAAA

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FIGURE 316

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAP
QEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

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FIGURE 317

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC
TGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA
GGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGGCATT
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG
GCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATTTAAGGT
AAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAAATCATTGT
CTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATGTTTACTCAA
TGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTTGAACATGGAT
CTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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FIGURE 318

MAYSTVQRVALASGLVLALSLLLLPKAFLSRGKRQEPPPTPEGKLGREPPMMHHHQAPSDGQTP
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILEFKVSRILILILHQ

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FIGURE 319

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG
GAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCT
GGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAATTA
CTATAGCACATTGTCAATTTACAACAGCAAACTATATGCTGAGTTTGGCAGAGAGGGCTTCTAA
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTATCAAGTTCAGTCAACAGAAGCATGGAGTGTT
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAGATAAAAT
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTAGATCCTCA
CTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG
AACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT
AATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG
ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGCAGAGCTTTC
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT
TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACCTCAAGC
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTTCAAGATGCTAGAGATATCTGGTACCTTGC
TGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTATATACTAGAGT
TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAA
CAGATAACATTTTTTTTTTGGTTTTTGGGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGA
AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCTATCTGTGA
GCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATAACAATATTACATTACAGCCTGTA
TTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAAGTTGTTGACATAAATTTGTAATGCATA
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCA
TTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCACATTTTA
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTTCATTAT
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACATA
GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAAACAACTACTATG
ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG
TACTTGTTCTAAGCAAATTAAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA
TAACAATAAAATATAAATCACCCA

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FIGURE 320

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKQLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYTNAVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

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FIGURE 321

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT
AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCCCGCAAGGCGGCA
TCTGCTGGTCCTGCTGCTGCTCCTCTCTACCCTGGTGATCCCCTCCGCTGCAGCTCCTATCCA
TGATGCTGACGCCCAAGAGAGCTCCTTGGGTCTCACAGGCCTCCAGAGCCTACTCCAAGGCTT
CAGCCGACTTTTCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT
GGACTTCCGGGGCCTCCCTGGGAACTACCACAAAGAGGAGAACCAGGAGCACCAGCTGGGGAA
CAACACCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAGCTGCCACGGCGGAGGTCCCACCAG
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT
GGACTCCGCAAGGGGACCCACAAGGACGTCCTAGAAGAGGGGACCGAGAGCTCCTCCCACTCC
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA
TAAAGTTCTTTCTTACATCTAAAAA

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FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): 2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLQGFSLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWIIKLPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGTKDVLEEGTESSSHSRLSPRKTHLLYILRPSR
QL

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-glycosylation sites:

Amino acids 97-101;112-116

N-myristoylation sites:

Amino acids 80-86;132-138;203-209;216-222

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FIGURE 323

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC
TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGCC
CAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC
TCCCTTACGGGGCTCACAATCGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTAC
GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG
GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG
ACTTACTTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTTCTTATCATTGTGGGG
ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGT
TTGCTTGTCAATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAAC TTATG
GTTCCAGTACAATGGTCAGATATGGTCAC TTTGAAAGCCAGGATGACAAATTATGGATTACCT
AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTA
GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTT
AGAGAATTTCCAGGATGTTCCAAACAGGCCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
GGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACA ACTGCAGGTGCTGAGGTTT
CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG
GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAAC
TCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA
CACACATCCATGGCAAACAGCTTTTAATACACACTTTGAGATGGAGGAGTTATATAAAGAAATG
TCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTG
TTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA
TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC
CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC
ACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA
TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT
AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC
TTCTGATGCTAAATAAATTATATATCAGAAAAC TTTCAATATTGGTGACTACCTAAATGTGAT
TTTTGCTGGTTACTAAATATTCTTACC ACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCT
GATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTTCAGTTCT
GATAATGTTAAGAATAACCAT TATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTGA
GCCTTTCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTA
TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA
ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAA
AGGACTTGTATGCTGTTTTTCTCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTTAAAA
AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTCTACAGA
AAATAGTGTCTTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAG
AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTT
TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTAT
TTTGTATTATTTCTCAGAATATGGAAAGAAAATTA AAATGTGTCAATAAATATTTTCTAGAGAG
TAA

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FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQWS
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTENDWPPDSCCVREFPGC
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

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FIGURE 325

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA
ATCACCATCTGAATTCAGAAAGCCCTGTTTCATGGTTGGGGATATTTTCTCGACTGCATGGAAT
CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTCTCTAT
GTCTCTTATCTGCGCTTTTGCTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCCG
TGTGTACTTGTACCAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT
TTTTATTACGCCATCGCTGCAGCTCTTGTTATTACATCGAACTCCTTTGATGTGATCAGTG
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTATAGAAAACAACAACATCAAGT
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCACTTGAGCCTTGCAAACAACA
ATCTCCAGACACTCCCAAAAGATATTTTCAAAGGCCTGGATTCTTTAACAATGTGGACCTGA
GGGGTAATTCATTTAATTGTGACTGTAACTGAAATGGCTAGTGGAATGGCTTGGCCACACCA
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCAGAATACAAGAAGCGCAAAATCAATA
GTCTCTCCTCGAAGGATTTTCGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT
ATCAATCATTGTCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC
CTTTTACTGGAAAATGCATTTTCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAAACTCAGCTCTATG
TTATTGTGGCCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTGCAAATAAAT
TCATAAAAATCCAGGATATTGAAATTCTCAAAATCCGAAAACCAATGACATTGAAACATTC
AGATTGAAAACAACCTGGTACTTTGTTGTTGCTGACAGTTCAAAGCTGGTTTACTACCATTTAC
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT
AGTAGTTCCCAGCGTCCTGTAATTTATCAGTGGAACAAAGCAACACAATTATTTACTAACC
ACTGACATTCCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAAGGGGACGTG
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCCAGCCTCTTCAAATAAATAAT
TACCAATATGCAATTCCTTGGAAGTGATTACTCCTTTACTCAAGTGTATAACTGGGATGCAGAG
AAAGCCAAATTTGTGAAATTTTCAGGAATTAATGTTTCAGGCACCAAGATCATTCACACATGTG
TCCATTAATAAGCGTAATTTTCTTTTTGCTTCCAGTTTTAAGGGAAATACACAGATTTACAAA
CATGTCATAGTTGACTTAAGCGCATGAGACACCAAATTCGTGGCTGCCATCAGAAATTTTCT
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAAATGAAT
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAAGTGTCCA
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA
GTGAAGATGTGTAAATAAGCGTTTAAATGGTATCTGTTACTCCAAAAGAAATATTAATATGTA
CTTTTCCATTTATTTATTTCATGTGTACAGAAACAACCTGCCAAATAAAATGTTTACATTTTCTT
TCATA

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FIGURE 326

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLTEGKKPAKPKCPAVCTCTKDNCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPQLLLFTSNFSDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLNANNLQTLPKDIFKGLDSLNTNVDLRGNSFNCDCK
LKWLVEWLGHNTATVEDIYCEGPPEYKKRKINSLSSKDFDCIITEFAKSQDLPLYQSLSID
TFSYLNDEYVVIAQPFTGKCIFLEWDHVEKTFRNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFVVDSSKAGFTTIY
KWNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNEMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMPSRGSMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLEASS
FKGNTQIYKHVIVDLA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235;378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

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FIGURE 327

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC
CTACCAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAGTGCTTGA
AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC
CAGAAGGATGCCCTCCATTCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC
CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA
CCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA
CTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCA
GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTG
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG
TCATTTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCAC
ATGCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA
GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGTGAGTG
TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA
TAACAATGGTGGCTGCAGCCACTCTTGCCCTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC
CCGGGGCCTGGTGTCTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAA
TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCTGACCAACAC
CTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCAAGACATGTGG
TACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA
GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC
CTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC
ACTGGAAATCATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAA
TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTT
TGGCATTGAGCCCCTGGTGCACGTGAGCGGCTTGAAAGCTTGGTGGAGAGCTGCTTTGCCAC
CCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA
TGAATCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT
CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTTCTGCACTGCCGGGTTCTTGTCTGTGGAGT
GTTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGGCGAATGCGTCTGGGGCAGGAGG
AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGA
GGACTAGTTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC
CCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTGAGACTTCACACTGTGAGTTTCA
ACTCCAGCACCAACTCACTCTGATTCTGGTCCATTCAAGTGGGCACAGGTCACAGCACTGCTG
AACAAATGTGGCCTGGGTGGGTTTTCTATCTTTCTAGGGTTGAAAATAAATGTCCACCCAGAA
AGACACTCACCCCATTTCCCTCATTTCTTTCTTACACTTAAATACCTCGTGTATGGTGCATC
AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAG
TTACTGAAATTATGACTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT
GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAACAGTAT
ATAATTTT

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FIGURE 328

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLQDESQGPPLCDNHVNGEWYHFT
GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG
GYVYRLTKPSVCFHVYCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRG
LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLFLTLNTSCRGVSNNGTHVNILFSLKTCGTV
VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE
IMSRNHGIFPFTLEIFKDNEFEFPYREALPTLKLRLDSLYFGIEPVVHVSGLSLVESCFATPT
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRVLVCGVLD
ERSRCAQGCHRRMRGAGGEDSAGLQGQTLTGGPPIRIDWED

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

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FIGURE 329

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT
GCACTCGGGCCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC
TGTGTGGGGAGGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC
GGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGGTGATTCT
TGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA
CAGGGAACTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTA
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA
TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCC
TGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG
AGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGACAAACAGCACGTCT
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCCATCCCTGG
CTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC
TCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGA
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTGATTGACAGCACACGGT
GCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGG
AAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGGCCCTGATGTACCAATCTGACCAGT
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCAGGAGTAT
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCT
GCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCAA
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCATTCTT
GGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCTCGCAGCCCAGAGGCGCCAGAGGAAG
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACT
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC
AGGCTGTCTTGTAAGGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCA
GCCCTGTCCGTCTTACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGG
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAA

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FIGURE 330

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNNSGPCLSGSLVSLHCL
ACGKSLKTPRVVGGEESVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDT
QGDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:
amino acids 32-53 (typeII)

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FIGURE 331

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGGC
TCCAGGACTTTGGCCATCTATAAAGCTTGGCA**ATG**AGAAATAAGAAAATTCTCAAGGAGGACG
AGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAATCA
ATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGA~~ACT~~TCTCCCTAGCTGTGGTGGTCATCTACC
TGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC
TCCGGGTCTTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGATCGAGGCTGCAAGTCC
TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAAC
TCACTCAGAACCCAGGGATGTTTCAAGTCAAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGTC
ACAAGGGGGCCATGGGCATGCCTGGTGGCCCTGGCCCGCCGGGACCCTGCTGAGAAGGGAG
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGGGCCACGGGGAG
TCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAGGAGCCACTGGCA
CCCCAGGACCCCAAGGAGAGAAAGGGCAGCAAAAGGCGATGGGGGTCTCATTGGCCCAAAAGGGG
AAACTGGAACATAAGGGAGAGAAAGGAGACCTGGGTCTCCCAGGAAGCAAAGGGGACAGGGGCA
TGAAAGGAGATGCAGGGGTCTATGGGGCCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA
GGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC
TGCAGGGTGTTCCGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA
GTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG
TTCCAGGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGGGCTGGCAGGTCCCAAGGGAG
CCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG
TAAAGGGAGAAAAAGGTGAAAGAGGTGAAACTCAGTGTCCGTGAGGATTGTGCGCAGTAGTA
ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCGATGACGAGTGGC
AAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTACTCCAAAGGAAGGGCCCTGTACA
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTGCGGGCACGGAGAGTA
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG
GCGTGGAGTGCAGCGT**CTGA**ACCCGGAACCCCTTTCATTCTCTGCTCCCGAGGTGTCTCGGG
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTTCCTGGGGACAACCTGAGCAGCCTCTGG
AGAGGGGCCATTAATAAAGCTCAACATCATTGA

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FIGURE 332

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQAGPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPGQPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGD
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPAGAKGDQGPGLQGVPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGGQGRKGESGVPGPAGVKGEQ
GSPGLAGPKGAPGQAGQKGDQGVKSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYSG
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVAGGTGQIWLNDNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 333

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG
CCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTTCT
CCATCCCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGGCTACCCTGAAGCTCTGGC
TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCAACTG
CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGTGGGAG
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGCAGACTA
TCAGGGTGCCGGCGGTGAGAAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCGG
GGCACTTGTGGGTTGCAGAGCCCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGCTACCAGGT
CCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC
CAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGAGCCTGGCCGA
GCTGCTGCAGGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT
GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGCACCAGTGGGGCC
ATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC
GTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGGTGTACAACCGCCAA
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCCTTTGCCAATGATCCT
GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGAGCCCTGGGGACCGAGTG
TCTCTGCGCTCGCTCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC
CTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAGAATCCAGCCCCTGACAACCTTT
CTTCTGCCCTCTCTTGGCCCCAGAAACAGCAGCAGGAGAGAGACTCCCTCTGGCTCCTATC
CCACCTCTTTGCATGGGACCCCTGTGCCAAACACCCCAAGTTTAAGAGAAGAGTAGAGCTGTGGC
ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACCTCCCAGCCACCTGCTGCATC
TGTTCTTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCAAGAAGGAAGATCTGCACTACTT
TGCGGCCTCTGCTCCTCCGGTTCCCCACCCAGCTTCCTGCTCAATGCTGATCAGGGACAGG
TGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG
CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA
GTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCCTTCTATGCTGGATCCCAGAT
GGACTCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTGCTCTGGCTGAGAGCA
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC
TCTTGCTTGGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC
TCTGACTGCTGCCTCCTTCCCTCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG
CATATCCCCACTATCTCTCTTCTCCTGATCTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCT
ATTACCTGGGATTCCATGATTCAATTCCTTCAGACCCTCTCCTGCCAGTATGCTAAACCCTCCC
TCTCTCTTTCTTATCCCGCTGTCCCATTTGCCAGCCTGGATGAATCTATCAATAAAACAAC
AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGA
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAACGTATACTAA
AATTAAAAA

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FIGURE 334

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECELVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRGNLL
GGWKYSSFSGFLIFPL

Signal peptide:
amino acids 1-32

FIGURE 335

[illegible]

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FIGURE 336

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIYVLYFTWLVFDWNTPKKGGRRSQW
VRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSMPGKN
AVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFH
GRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQDDIDLYHTMYMEALVKLFDKHKTKFG
LPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 337

[illegible]

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FIGURE 338

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVFVVSGLVINFEVQLCTLALWPVSKQLYRRLNCR LAYSLWSQLVM
LLEWWSCTECTLFSTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQGMFPGEQFKPARRPWTLLNFLSWA
TILLSPLFSFVLGVFASGSPLLILTF LGFVGAASFGVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

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FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTCTTCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCTTTCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAAT
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGATGCTGCTCCTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGAACCCCATCTGTACTAAAAATAACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAAA

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FIGURE 340

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCF SFALALGH FLLISLVGKGLSLSCGVGGRQAGLR LIRPWVRRE
GKINFY TNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFS LFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

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FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTCGCGGCGGCCGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTGTTATTTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

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FIGURE 342

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPEMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTIVQ

Important features of the protein:**Transmembrane domain:**

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

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FIGURE 343

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCAAACCTGACCTTCACCTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGACA**AGCCCCGAAGATTTTCATAGGCG
ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTT
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG
TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGC
ATTGAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTGGCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTATGGTTATTT
GTAA

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FIGURE 344

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD .

Signal peptide:
amino acids 1-15

FIGURE 345

[illegible]

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FIGURE 346

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61; NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSDSDSVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEKQQ
AKPVKVERTKRSEGFMSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEKLAGEEELAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

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FIGURE 347

GTGTTCTCTCTGGATCTTCACCTTACCACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAGCCAAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATTGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTTGGGTTCATC
AGAAGGACTGGATTTTCAAACCTCTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAATTTTAAAGAAGATTATTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAAGTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCCTACTCATGACCACCCTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAATTTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCTATTGCAAGATGAGGAGTACGGA
TGTAATGTTTCTTGGAACAGACATTGGAAGTGTCTCAAAGTTGTGTCAGCATTTCAAAGGAAAGTGGGAATATGGA
AGAGGTAGTGTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
GCAACAATTTGATCATTTGGTTCCCGAGATGGATTAGTTCAGCTCTCCTTGACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCCAATCACCCAGTGTGGACATCGAAGACAG
CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAAGAAGAAGGATTTGGGATGTATTACTG
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGCGACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAAGGGCAAAAATTCATTGAACAGTTTTT
CCAAGAACAAATCTTGCAACAAGCAAAGTATAAGAATTATCCTTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTTTGAATTTATTGTGATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTCCCTCGAATGTCCATTAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACCTCCATTATC
AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTAATAAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAATCACAATAAAGTGAAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC
AATGATATTTAGTATATATTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC
CTTTATCTCTCCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAAAC
AACGGAAGGGTTAAATTAACCTTTGACATCTTCACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAAT
GTAGTATTGTTTTTGAATTTAACAATAAATAAGCCTGCTACATGT

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FIGURE 348

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPRLKLTYSKDLLLSNSCIPFLG
SSEGLDFQTLTLLDEERGRLLLGAKDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRCLKCPFDPPQ
PFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHYYIRTDISEHYWLNAGKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLICSIPGS
DGADTYFDELQDIYLLPTRDERNPVYGVFTTTSSIFKGSACVYSMADIRAVFNGPYAHKES
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFK
RINVYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSSISKEKWNMEEVVLEELQIFKHSS
IILNMELESLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNACSRYPATSK
RRARRQDVKYGDPITQCWDIEDSISHETADEKVIKGFIEFNSTFLECIPKSQQATIKWYIQRS
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLNVIENEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGKGPWKHMQEM
KKKRNRRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

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FIGURE 349

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACC GCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCCACCAC
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGA CTACAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTCATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTCTATGGAGCTACAGAGGGGAGGGAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGACTTCAATTTCCCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCGGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGTTGAGTGGCTGGAGGTGATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCGTCTGCTGCCCGGGCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAATTTGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGGAAGAGCTGCTTGGCCCCC
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCGTCCCCTTCTCCTCCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACC
CAGATCCCTCACCTGAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTCAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCCAAGGT
GGAACTTGCCCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTTCCCATTTGTTCTATCATCTCTAGGACC
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTTCCACCCCTGGCTCCATGACCCACCCCACTCTGGATG
CCAGGGTCACTGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCTCTTGTG
CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGGCCACCACGGGCAGGGGCTGCTCCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCCFGGGCTCCAGGACCTTCCCTACCTCCACCACCAAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCAGTGC
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTCTTGGCTGCCCATTTGCCCTCTGAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCTTCAAGTG
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCAACCCCTG
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCTGTCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTCTCTTCTGGAGCGTCCCTGACGGACAAGTGGAG
GCCTCTTGTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
CCTCCTGCAGGCTGGAGGTGGCATCCCACTGGACAGCAGGAGGAGGGAGTGAGGGTAACATTTCCATTTCCCT
TCATGTTTTGTTTCTTACGTTCTTTTACGATGCTCCTTAAACCCCAAGCCCCAATTTCCCAAGCCCCATTT
TTCTTGTCTTTATCTAATAAACTCAATATTAAG

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FIGURE 350

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCCLPNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSPSSQSDSNPCGAEPFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```


FIGURE 351A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCCACAGAAGCGGCCAGACAGAGTCTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAGAGGGGCTCAGGAGGAGAGTTTGGAGAACGACCCCTGG
GCACCTCTCCCAAGCCCAAGGATTAAGTTTCTCCATTCTCTTAACGGTCTCAGCCCTTGTGAAAACCTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAGCTAGGGTGTGGAGGACTTTGGT
GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCATGTCCTCCAGACAGGCTCGCATCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCCAACCTGCCCTCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCTCTCTCTGCCCCACGCCCGGCTGGCCAGCCCCCTCCCCCGGGAGGAGAGAT
CGTGTTTCCAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA
GGCCTTTTGGGAGAGCGCTGCTACTAGAGCTGGACAGGACTCCGGTGTGCAGTGCAGGGCTGACAGTGCAGTA
CCTGGGCGAGGCGCTGAGTCTGGTGGTGAGCAGAGCCTGGCACTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAACGCCA
CCTCCAGCCCCCTGGAGGGAGGCCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATTGTGCAACGTCAAGGCTCCTCTTGGAAAGCCCCAGCCCCAGAACCCGAAGAGCCAA
GGCGCTTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGGCACTGACAAGATGGCCGCTATCCACGGTGC
GGGCTTAAAGCGCTACCTGCTATAAGTGTATGGCAGCAGCAGCAAGGCCTTCAAGCAACCAAGCATCCGCAATCC
TGTGAGCTTTGGTGGTGAATCGGCTAGTGATCCTGGGGTCAAGCGAGGAGGGGGCCCCAAGTGGGGGCCAGTGCTGC
CCAGACCTGCGCAGCTTCTGTGCTTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CACAGCCATTCTGTTTACCCCTCAGGACCTGTGTGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAATCGGGTCACTGCTTCAACATGCTGCTGACAACCTCAAGCCATGCATCAGTTTGAATGGGCTTTGAGCAC
CTCTCGCCATGTGATGCCCCCTGTGATGGCTCATGTGATCTCAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT
CATCACTGACTTCTTGACAAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTGGGGCCGACTCACGCCATTGTCC
ACAGTGTCCCGCCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA
CTCGCCCTGGGCGGCTGACACACCTCGGGGGCCGACAGGCCCTGCATGGGTGGTGGCTGCCCTCCACATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGCTCTGGGGACCATGGGTGACTGCTCTCGGACCTG
TGGGGGTGGTGTCCAGTTCTCTCTCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCGGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCTACAACCACCCACCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTTCCTGCTACAC
AGGCGTGGCCCCCAGGACCATGTGCAAACTACCTGCCAGGCCCGGGCAGCTGGGCTACTACTATGTGCTGGAGCC
ACGGTGGTAGATGGGACCCCTGTCCCCGAGCAGCTCTCGGTCTGTGTCTCAGGCCGATGCATCCTATGCTGG
CTGTGATCGCATCATTGGCTCCAAGAAAGATTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATTCAAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
CATTCTTGTCCGGCAGCAGGGAACCTTGCCACCGGAGCATTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACCGTGTATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCTAGTCAAGTTGCGCTA
CAGCGGGGCCACTCGAGCTCTCAGACACTGTGAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTT
AGTGCTGGCAACCCCGAGGACACGCTCCGATACAGCTTCTGTCGCCCCGGCGACCCCTTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG
GAAAATAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCAGTGATGGTTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAACTGCCCTCTGCCCTGGGGTCAAGGAGGGAGGGGGAAGCAGGAGGGGCTGGGCCC
CAGTTGTATTTTATTAGTATTTATTTCACTTTTATTTAGACAGGGAAGGGGACAGGACTAGGGTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCCTC
TTCCTGAATTTTATTTTTTGGGAAAAAGAAAGTCAAGGGTAGAGTGGGCCCTCAGGCGAGTGAGGGATTATCTTTT
TTTTTTTTTTCTTTCTTTCTTTCTTTTGTGAGACAGAACTCGCTCTGTCGCCAGCTGGAGTGCATATG
GCATAATCTCGGCTCACTGCATCCTCCGCTCCCGGGTTCAAGTGATTCTCATGCTCAGCCTCCTGATGAGTGC
GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTTGTTTTGTTTTGTTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTTCAGCAATTCTCCTGCCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCAAC
CATGTTGGCCAGGCTGGTCTCGAATCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAGTGCTGGGATT
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCACTAATTTTGTATTTTTAGTAGAGACAGGGTTTCAACATGT
TGGCCAGGCTGCTCTTGAACTCCTGACCTCAGTAACTGACCTGCTCGGCCCTCCCAAGTGCTGGGATTACAGG

FIGURE 351B

[illegible]

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FIGURE 352

>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLLASLLPSARLASPLPREEEIVF
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAAAKA
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL
FTRQDL CGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNGGKYCEGRRTFR
SCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPDVLPGA
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPDWLH
RRAQILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

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FIGURE 353

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCCCTGC
TTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAA
GACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA
TAACAAGTTTAAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 354

MASTAVQLLGFLLSFLGMVGTLLTTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQDEA
PYRPFYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 355

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
AGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCTCC
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGG
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
GGCAGAGTTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC
TGCAGGCAGTGCAGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
GGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTTGGGCTGGGTG
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAG
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTGCCTACAAGCCTG
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
GTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCAGCACTATGTG**TAA**TGCTCTA
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAA
CTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG
ACTCCCCCTCTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCCAGCTTATCCCCAAG
AAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAAGATATT
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA
AAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGTGCGGGGTCAGAAA
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAATTTAAGTCCTAAATATAGTTAAAATAA
ATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
AAGGAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
GTACAAATTCCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATACACCTGTAGTCCCAGCATTCCGGGAG
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGA
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

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FIGURE 356

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

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FIGURE 357

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGG
CTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA
GTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAACTTCTGGGAAGGACTGTGGATG
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTCATCCCT
GTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTGATTGTTGGA
GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
CCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC
AGAAGTCAGTATGTGTACTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACA
AAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGC
CTAATCTTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAA
TGAGATATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
TTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCA
CATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAGTCCATTACACTGAATAAAT
AGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG
TTTAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAAATGAAGGCTTTAA
TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA
ATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT
TTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTTCCAGGGCTATACTC
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAATATTTTT
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT
GTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATGTCATTTTTGTTCTGTGAAAAATAAATTTT
CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT
CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTGCGACGTCTGTCTAGCTTAAAT
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

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FIGURE 358

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQ
CKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

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FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACATATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTACGAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTTTGATATTTTAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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FIGURE 360

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFLG
SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYDED
SAIGPRSPYGFRHGASVNYDDY**Signal peptide:**

amino acids 1-30

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FIGURE 361

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC
AGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG
GACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAAGC
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC
TGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGATTGTGTCC
GGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGGCCACTCTCC
TACTGGCTGACAGGATGCCGCCTGAGATGAACAGGGTGCGGGTGCAACCGTGGAGTCATTCCA
AGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCACTTCATGTTAT
TTTCTTCCCTTCCCATTACAACTAAACTGACCAGAGCCCCAGGAATAAATGGTTTTCTTGG
CTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGG
ACCACAATAAAGAAATCTTTATATTTATCG

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FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN
ENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHCAKRIVSGARGMNNW
VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

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FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCTAGCCCTGCTTGACTGAGAACCCAC
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGAAAGAAACACCTGAGCA
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT
TTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACGCTGTTG
GGTGAAACTTGGGTCCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACGCTGTTG
GCAAATGTCAGGACCAGGTAAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
AGTTCTCTCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGTTGCACCCCTC
CCCACCACACCTGACACAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
ACAGCCCTCTGGAGGGCCTGCCACCCCTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG
TGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
TCAAGGCAAGGAGGAGGAGGATAAGGAAGCCCCAAAGAGGGGACTGGGGGGCTGATGAGGACG
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAAGCCTGGACCCACGTGGCCTCCAGGAGG
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC
AGCAGCACCCCTCAGGACAGCCTGCCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCAGGGCCTTCTCTGAAGG
AGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT
GCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC
GTGGGGTGTGGACTGGAAGCTGGATTTCCTGGAACCTTTGCCAGAGCATGTGAGGAAGG
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG
ACAGACATTACTTCCAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTGGTGAAG
ACCTCGAAGTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
GGGTAGGACACATCTACCAAATCAGGATTCCCATTCCCCCTCGACCAGGAGGCCACCCCTGA
GGAACAGGGTTTCGATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
GCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGACGCTGC
AAAGGAGACTGGGTGTGCGGACATTCCACTGGTTTTCTGGCTAATGTCTACCTGAGCTGTACC
CATCTGAACCCAGGCCAGTTTCTCTGGAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGCACTGACAGCC
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCACAGCACC
TGTGCTTTGCTGTGAGGAGGAGGAGGATTCTTTCAGAACTGCACGGAGGAAGGCCTGGCCA
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTTGGGAAAT
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
CCCGCCAGCAGTGGCGATTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTCAG
AAGGAAAAGAGAATTTTGGCCATCAAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA
GAATATAGGAAGTTTCTCCTTTTACACCTTATTTCAATTGACTGCTGGCTGCTTA

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FIGURE 364

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLFVMDAHCECHPGWLEPLLSRIAGDRSRVVSPVIDVI
DWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATLRNRVRIA
ETWLGSEFKETFYKHSPEAFSLSKAEKPCMERLQLQRRRLGCRTFHWFLANVPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER

Signal peptide:

amino acids 1-28

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FIGURE 365

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGC
AGCCGGGAGCCATGCGACCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG
AATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA
CACTGTTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGTGTTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAAATTATTTCCAACA

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FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLOGPAGVP
GRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 367

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACC GCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT
GCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTTGAAGCGAATAAAGGGGCCG
CGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 368

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDGTP
PAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

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FIGURE 369

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGCGCTGGCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAAC
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTCACCGACTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG
CTGGGAGTGTGTCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG
GGACCCCTTCCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTGAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAGACTCGCAGCTCG
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGGCCCTAC
TGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCTTCCACCTGGCTGTGATCGG
GTAGGGCGGGGCCGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGTCCACAGGTCTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAACTGGCACAAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGG
CACAGGCTGGCTCCCTCAGCTCCCACGTCCCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCTCAGCTGG
AGGCGGGCATCTTCTTAAAGGGTCCCCATAGGGTCTGGTTCACCCCATCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCCA
CATTGCCTTTTACAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGCACGAGGGTGTGCTGGATGTGGCCACAC
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCCCT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

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FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE
LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL
APGSWGGGQLSREGPSLAPEGSMPSPRGDL P

Signal peptide:

amino acids 1-15

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FIGURE 371

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCCC
CCGGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGGCTGCCGCCTC
TCGGCCACGGCTGGGTTCGGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGGCCCCGACCCTGAGGGCGTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCAGAAAAAGAATATGAAGGTG
AAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA
AAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT
TCCATGACTTGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAAA

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FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQ RAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 373

GACTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTCAAACCTGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCCAGTTTGGAGGCCTGCCCCGTGCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGAAAAGTGACGTCAGTGATTCTTGGCCTGAAC
AACATCATTGACATAAAGGTCACTGACCCCCAGCTGCTGGAACCTTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTCAATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

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FIGURE 374

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533

><subunit 1 of 1, 256 aa, 1 stop

><MW: 26713, pI: 5.62, NX(S/T): 0

MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSPVPLNNIIDIKVTDLPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHLVLGDC
THSPGSLQISLLDGLGPLPIQGLDLSLTGILNKVLPVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

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FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAATATGTCAAGATCCAGACTTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAA
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTGGTGGC
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTATTATGCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

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FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99; NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP
APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

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FIGURE 377

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCC**AT**GGCCAGGCCCGGC
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGGCCTCGGGGGGCATCGGCGCGGCC
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCTACAGA
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGC
ACCACTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
GCCTACCACTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACG
TGCATCTCTCCAGGTGTGGTGGAGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAG
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCCTTCATGGCTTGCCTCCTG
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCTGTCCACACCCCGACC
AGGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
TGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTGTTCTTG
TGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
GTGGCCAAAATCCCCATCTTCTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
GAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCAGTCTTGGCTTCTTGT
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
CCAGTGGATTTTCATGGTGATCATTAAGAAAGAAAATCGCAACCAAAAAAAAAAAAAA

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FIGURE 378

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT
LIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFN VNV LALS
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

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FIGURE 379

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGCGACCGTGACGAGAAGCCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACTCCCT
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGCTTACCT
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTTGCTTCTTCAGAAATGTTTTTACAATCTC
AAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTTGTTGGACTCATTGGGGATT
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGG
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAACCTCTAATTCTGTACATA
AAAAATTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACTTGTTGATGTGGTAAGCAGATAGGTGAGTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCAATTTCTATAACACATTTAT
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTAATCATTCTGTCATTTGTTCTC
AATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTGTT
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTA
AAAATTACACTTATAAGAGTATAATCCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAATAATAGTTGTAAACTCTAATCTTATACTTATTG
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTTACATACAT
GAATGTTCAATTTAAAAGTTTAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC
ATATTTGGGTTAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTGCTTG
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAATAAGAACATTTAAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA
ATTCTAGTATAAAACAAATTATACTTTTATTTAAATTTCCCTTGAGCAAATCTAATTGCCAC
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTGTCGTCATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTAAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

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FIGURE 380

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP
VTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

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FIGURE 381

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGG
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTTCAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAATGAGGAACCTGAGAAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT
TTATTTTTTTATTCTTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAACCTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAATGACAGGA
TTTCGTTCTTAATTTCAATTAAATAACCACACATGGCAAAAA

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FIGURE 382

MGLLLLVLFSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQ
PVKGHGTLGESPMPPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTTCCTTCAAGTAGCACCTCTATCAG
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
GCTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAAC
ACCAAATAAATAATGCTGGGATTCCTTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT
ACCTATACCACAACAGTTTAGATGAATTCCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCTATCTGG
AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCCGAG
ACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTT
TGCCAGGACTATAGAAGAAGTACGCTTGATGATAATCGCATATCCACTATTTTCATCACCAT
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG
GTTTAGGTGACAAAGTTTTCTTCAACCTTAATTTGACAGAGCTGTCCTGGTGCGGAATT
CCCTGACTGCTGCACCAGTAAACCTTCAGGACACAAACCTGAGGAAGCTTTATCTTCAAGATA
ACCACATCAATCGGGTGCCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTGACTGGATA
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATAAAC
AACTGATTTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTT
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA
GCACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAG
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATA
TCTCTTGAAACTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATA
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
CAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
ACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTTCGAATGTACAACC
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG
CTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGT
ATGTTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAA
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTT
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCA
TATTTCTCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

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FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEEPTNLPKYVKELHLQENNI RTITYDSL SK
IPYLEELHLDDNSVSAVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLT AAPVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDL DNITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ
GQWPAPVTKQPDIKNP KLT KDQQTGSPSRKTITITVKS VTS DTI HISWKLALPMTALRLSWL
KLGHS PAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCIETETAPL
RMYNP TTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIAL LALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSES
SSNRSYRDSGIPDS DSHSHS

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645**Amidation site.**

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

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FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG
CAGCCCTGCCGGGCCACTTGTCTTCATGCTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG
GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA
GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCCTAGAACAGAGGCTGCCTGAAATCAACCT
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC
CCAGGAGCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
GCTGACCCTCCAGCCCGGGTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTT
GGTGTACCCACGTTCTGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG
CCTCATGACCAAGCCCGGCTGCTCAGGCTACTGCCTGTCCACCAACTGCTCTTCTTCTCTG
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCTACCTACCCG
GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTATATTTTTTTAGTAGAGAC
AGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC
AGGCTCCCAAAGTGTGGGATTATAGGTTGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAAA
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCCTATACA
TCCTGGCAGAATAACCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA
GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

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FIGURE 386

MSARGRWEGGRRACRGSGLARAQGAERVTSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL
SLRVGMLGEKLEAAIQRSILHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCSRLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIQYAYPTRDIFMENIMFCMGGGFSDFYKLRWLEAILS
WQKQQEGCGFGEPAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSCLILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

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FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTTCATGATATACCTTCTGGATCTTATGTAAGTGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTG
GCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAGTGGGGCTGGCAAAGGAGGTAGTCAG
GCCGTCCAGAGCTGGCATTTGCACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGGAAAA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACTGTGTATGTT
AACTTTTGTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAA
TTATATGAACACTACTATACATTATGTATATTAATTAAAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 388

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWIS
AARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVS PAYRFD PVRVDITSKGKMRARYVNYI
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

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FIGURE 389

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATGG**CGTGGAGCCTTGGGAG
CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG
AATGAATTCTGTAAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
CCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGACACCAT
TATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
CCCTAAAAATTGAGAATGAATACGAACTTGAGACTATGAAGAATGTGTATAACTCATGGACTTA
TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
TGAGGTCCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTCGAGGGTTTCTTCC
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
GGTCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACGCCTTCTCCCTAG
GAATTCCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
TTTCTCCTTTCCATTGTGCGGATGAGAATGATGTTTTTGACAAGCTAAGTGTGATTGCAGAAGA
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCCTGGGCAGGG
GCCCCAAAGCT**TAGG**CTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGCA
AAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCATGATGTTTTTCAGAAGTTGGC
CACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG
ATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
AGAAACAGAAATACTTAAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
GCTACACAGAGCACGGACTTTTGGATTCTTTCAGTACTTTGAATTTATTTTTCTACCTATAT
ATGTTTTATATGCTGCTGGTGCTCCATTAAAGTTTTACTCTGTGTTGC

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FIGURE 390

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVEQTTHDETVPSPWMVAVILMASVFMVCLALLGCFSLLWCYKKT
KYAFSPRNSLPQHLKEFLGHPHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDSCSL
GTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

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FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCC
AGATCACTGAGGCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCAACATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGTGAAATAAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC
GGCGATGCACTCGCACTGCAAATGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTTACAGATAAGGAAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

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FIGURE 392

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

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FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTC
TGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCACACCCTGCTGGAGTTCTACTTGAAAACTGTTTTCAAAAACCACCACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTACTCTGGCCAACAACCTTTGTTCTCATC
GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**TGA**ATGTCTAGA
CCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCATTTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTTAATTAATGTCAGTATTTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTTGGCCTGTCTTTGGATTGTAAAAAACAGAGAGGGATG
CTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTTCAATTTCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAA
AAAA

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FIGURE 394

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLWSQVSGAQQQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLLKTVFKNHHN
RTVEVRTLKSFSTLANNEVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL

Signal sequence:
amino acids 1-42

N-glycosylation sites.
amino acids 85-89, 99-103, 126-130

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FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTCTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTT
TGAAATTTCAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGTGCTGAGGTTTGGGGT

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FIGURE 396

MFRSSLLFWPPLCLLSLFLILISSIYSECKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTG
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTCTATCCTTTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACAGTGGAGTCCCT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGGAGGAGGTGTCCACACAAGGAACATT
CAGAACAATACCCCCGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATAACCCCC
TCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTGCAGTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTTATATGTGCAGATGGAAAAC**TGAT**GCCAACA
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGAGTGTCTGTGAGAA

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FIGURE 398

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHHPANLILYGNFDRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGETSLTQQESLS
RTIPDPKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP
QLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

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FIGURE 399

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGAC
TATTC AATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTCACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGACAGCTG
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT
CTTGTTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTCAGAGAAGTGAGGTCA TCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCAT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG
TAG

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FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRLDRVEFPVTTSVATGDYS
ILMNVS WVL RADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTF SYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTP
YFPTCGSDCIRHKGTVVLCPTGVFPFLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP
VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL

Important features of the protein:**Signal peptide:**

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

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FIGURE 401

GGGAACAGGGAACTATCAGCCCGTCGGCCCTCCGGGGCCCTGCATTCTCTAGCCATGGACCG
GGACCTTTTGCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG
CGAACAGCAGGACAATCCCACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCG
GGGCCCCGCCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA
GATACAGAAATTCATCTCCAAAAAGCGGATCTGCTTTTTGCACTTTCCTGGAAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTCATGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGGAATTCGGTTTTTTCAT
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAAATGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCTTTATACACAGGAGAAGTGTGAGCTAAATGCAATTTC
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTTCCTTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAAACAATC
CGCATCTTGGGCTTTTAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCATTAGAAAAGTGTCCAATCACAGAAATGCAAGAAAATACCTCTGCCA
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTCAAGTGTTCTTC
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTCTTCTGGTCACAAAAGGCATAA
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCCAGAAGGCATTCTCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCCAGCTAATAC
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGTACTCCTATTTATTTAAAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTCTATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAACAAAAAAATTA AAAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAATTTTACAAAATTA AAAATGTTTAAAGTTAAAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAATTATTTTTATGAATTTACTGT

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FIGURE 402

MDRDLLRQSLNCHGSSLLSLLRSEQQDNPHFRSLIGSAAEPARGPPPQHPLQGRKEKRVD
NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF
RDIERGDIVIGRISSIREFGFFMVLIICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSSLGFVNPGVVEFLLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGS LNKA
IEDFELALENCPTHNRNARKYLCQTLVERGGQLEEEEEKFLNAESYKKALALDETFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKRRRKSTSSSS
VSSADESVSSSSSSSSSGHKKRHHKHKRNRSESSRRHSSRRASSNQIDQNRKDECYPVP
ANTSASFLNHKQVEKLLGKQDRLQYEKTQIKEKDRCPLSSSSLEIPDDFGVYSYLFKKL
TIKQPQAGPSGDIPEEGIVIIDDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292;508-512;542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304;472-476;473-477;517-521;598-602

N-myristoylation sites:

Amino acids 218-224;222-228;271-277;348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

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FIGURE 403

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATA
GGAAAATAACTTGGGATTTTATATTGGAAGAC**ATG**GATCTTGCTGCCAACGAGATCAGCATTT
ATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCCAACTGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCGTGTTGGAGGAAGAGATTCAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCAAGTGGTGGCGCTGCT
TTCTTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC
TG**TAG**GAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAACAAAACGATGAACTGCAAAA

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FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPOYPLLIVVYK
VLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPPIAKKYMSENKGVPLHG
GDEDRPFDPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFFPYPWRRPLNRSQMLRELFVFTHL
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFTIGSGEAMLQLIPPFQCRRHCSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCTGGACTCCC
GTCTCCTCCTGTCTCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT
CAGCGGACGACCCTCTCGCTCCGGGGCTGAGCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG
TTTGGCTGCTGCTTCCCGCCGGGTGCCACTGCCACCGCCGCGCCTCTGCTGCCGCGCTCCGCGGGATGCTCAG
TAGCCCGCTGCCCGCCCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGTGCTGCAGAGTTGCACGAACTAGTC
ATGGTGCTGTGGGAGTCCCCGCGGCAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGTGGCTGCTGCTGCTG
CCCGTCATGCTACTCATCGTAGCCCCGCGGTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGAAGTGCCTAAACG
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAAA
TTTGATGGGGAATGTTTAAAGAATTGGAGACACTGTGACTTGCCTCTGTCTCAGTTCAAGTGCAACAATGACTATGTG
CCTGTGTGTGGCTCCAATGGGAGAGCTACCAGAATGAGTGTTACCTGCGACAGGCTGCATGCAACAGCAGAGT
GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
TCTGGAGAACTAGTCAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAAATGTGACGAAGATGCC
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCCTCTGCGCTTCTGATGGGAAA
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
CGATGTCAAGATAACACAACACTACAACACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGCCAGGTGTGATGCTGGTTATACTGGACAACACTGT
GAAAAAAGGACTACAGTGTTCTATACGTTGTTCCCGGTCTGTACGATTTTCAGTATGTCTTAATCGCAGCTGTG
ATTGGAACAATTCAGATTGCTGTCTGTGTGTGGTGGTCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
ATTACAGACAGAAGCAAAATACAGGGCACTACAGTTCAGACAATAACAAGAGCGTCCACGAGGTTAATCTAA
AGGGAGCATGTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
GACAAGAGATCTACACATGTTGCCTTGCAATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTTCTGTAATGTAAATAAACTATTTATA
TCACACAATATAGTTTTTCTTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG

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FIGURE 406

MVLWESPRQCSSWTLCGFCWLLLLLPVMLLIVARPVKLAAPPTSLSDCQTPTGWNCSGY
DDRENDLFLCDTINTCKFDGECLRIGDTVTCVCQFKCNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTTTTK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRCDAGY
TGQHCEKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTTRASTRLI

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FIGURE 407

CTCGCAGCCGAGCGCGGCCGCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
GTCCAGACTGAGGCCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCAATTTTTAA
CATTCCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCTCTCCACGACT
CGCTCGGCCCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCAGAGGAGGCCGACGTGCC
CGAGCTCCTCCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
TCTTGGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAA
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
ACCAAAATGGCGGGTATTTATGCATTCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGA
ACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
ACTATCCCAGCATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC
AATGTGTGGATGTGGACGAGTGTGCAACAGTCTCCACCAGTGCAACCCACCCAGATCTGCA
TCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGAGGATATTGGCTTCTGGAAGGCCAGT
GCTTAGACATTGATGAATGTCGCTATGTTTACTGCCAGCAGCTCTGTGCGAATGTTCTGGAT
CCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATG
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTCTCA
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTTATTGCAGTGATATGGACG
AGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCT
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
GTCTGTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCAAATGCAAGCCACGACCCGCTACCCTG
GGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
TGGACTTGGAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC
TGCGGATATATGTGTCGAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
TAGGCATTTTCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTA
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTTCTATGACACAGTTATCAAA
AAGTATTATCATTGCTCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGT
GAACAGCTTGCTGTCACTTCTTCACCTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA
AAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCTTTTTGCGTACACAGAGAA
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGC
CTGGTATTTTCAACCATAAAAGAAGTTTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATTCT
GTCTTGTTCAATTTTGAGTATTTTAAAAAATATGTCGTAGAATTCTTCGAAAGGCCCTTCAGA
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTCTTT
GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTACCCAATTGGATTGGAATGCAGAGGTCT
CCAAACTGATTAAATATTTGAAGAGA

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FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

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FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTCA
GGGAGGAGCACCAGCTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
TCGCTGGTCCTGTTGATGCCTGGCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGCTGGG
AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGAAGAGT
TATGCCGGCTTCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGCCGGGAGGTTCA
TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCAACAAGTAACATGACCTTGCCT
GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA
GGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT
TTATACAGTGCAGTAATTTCAGTTTTTCCAGATATTTCTGAATATAAAAAATAATGACTTTTTAT
GTCAGTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC
AACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
CCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCTTGTGGATGAGAAG
CAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
TTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT
CAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
CAGACTTTTAATGATGGAATATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACTGGAC
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCAG
GAATACAAGAAGGCAGAAAAAAAAGTTTTGGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
TACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT
CCTTATGTTGGATTAATACTACCTTCCCAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
TTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTTTTTGGGGGGAGATGTTTACT
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTTA
ATTTCTTCTAAGAGTAAGTGAAAAGTGACAGTTGTAACAAACAAAGCTGTAACATCTTTTTCTG
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAAATATTATTGGATAAGAATAGCTC
AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAATGTATAA
AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA

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FIGURE 410

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSLV
GPFPGGLNMKSYAGFLTVNKTYSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVTSNMTLRDRDFPWTTLTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQQFFQI
FPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDGYSDPESIIGGYAEF
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGTGCSNYY
NFLRCTEPEDQLYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLTEIMNNY
KVLIIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQAGDFHQV
IIRGGGHILPYDQPLRAFDMINRFIYGKWDYPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

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FIGURE 411

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGAGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCCCCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCCCAGCTCAGCGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGCTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCGCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCGGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCGAGGCCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGAGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGCTCCTGGGACCTCACTTTAGTCTTGGTATTTATTTTTCTCCATCTCCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTTCAAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGGCTGCCTTTTCCCC
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCCAG
CCATGGGACGGTCACCCAGCAGTGGCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA
AAGGCCAGGCCTGGAGCTTGCTCTCAGTTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTTTAAAAAAGCTTTGAAATGGATGGTTTGGGTATTAAAAAGAAAAAAGCTTAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCTGGGGAGGGAGGTTTTTTTGTGTTTTTGGGTTTTTTTTTGGTGTCTTGTCTTTCTCTCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGATGAACGGTGCTCCATTGCGACCTCCCCTCCTCGTGCCTGCCCTGCCCTCTCCA
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAA

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FIGURE 412

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDTVFDLVELEVLKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNSLSKLPQVVTDVGVHLQKLSINNEG
KLIVLNSLKMANLTELELIRCDLERIPHSIFSLHNLQEIIDLKDNNLKTIEEIIISFQHLHRLT
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAAATGAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAAG
AAAGGGAAGTATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCAGATTTTC
ATTCGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGGATCTCA
AAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTTTTGACACCA
TGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGAGTGGGGCAA
AAATACAAAATCAGATTTCCAGAAAATGCTCATCTGCATCTAAATACTGTCTTCTTAGGAT
TCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCATCTTAAACACAACAAAATGCACA
TTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGCCTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACTTTTTCAGATCCGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTACTCAAATCTTGACACCA
GAACTATAAAATTTGGAGCATGTACATTTAGAGTGTTTTACATTCAACAGGATAAAATCTATT
TGCTTTTGAACAAAATGGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTCGAATATTTAAATTTTGCCAATAATATCTTAACAGACG
AGTTGTTTTAAAAGAACTATCCAACCTGCCTCACTTGAAAACCTCTCATTTTGAATGGCAATAAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACACCCTTGGAACTTTGGATCTGA
GTCAAATCTATTACAACATAAAATGATGAAAATTTGCTCATGGCCAGAACTGTGGTCAATA
TGAATCTGTATACAATAAATTTGCTGATTCTGTCTTCAGGTGCTTGCCCAAAAGTATTCAAA
TACTTGACCTAAATAAATAACCAATCCAACTGACCTTACCTTAAAGAGACTATTCTATCTGATGGCCT
TACGAGAACTAAATATTGCATTTAATTTTCTAAGTATGATCTCCCTGGATGCAGTCTTCACTGA
GACTTTCAGTTCTGAACATTGAAATGAACCTTCATTCTCAGCCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAACTCTAATGCGGGAAGAAATCCATTCCGGTGTACCTGTGAATTA
AAAATTTTCATTAGCTTGAACATATTTCAGAGGTGATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATACCCCTTTAAACCTAAGGGGAACCTAGGTTAAAGACGTTTCACTCCACGAATTAT
CTTGCAACACAGCTCTGTTGATTGTCACCATTTGTTGTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATTGGCAGAGGTTAGGAAAACAACCAAGAACAACCTCAAGAGAAATGTCCGATTCCACG
CATTATTTTCATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTGATTTGCCTTTATGAAAGCTACTTTGACCCTGGCAAAAGCA
TTAGTGAAAATATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTCTACTTTGCCCACCACAATCTCTTCCATG
AAAATTTCTGATCATATAAATTTCTATCTTACTGGAACCCATTCCATTCTATTGCATTTCCACCA
GGTATCATAAACTGAAAGCTCTCCTGGAAAAAAGCATACTTGGAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCA
GAGAAATGTATGAACTGCAGACATTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTATAAAATCCCACAGTCTTGGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACCTTTATGATGGCAATTTGACAATATTTATTAAAAATAAA
AAATGGTTATTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGAAAAAGGTGTTTCATCCAGGATTGTTTATAATCATG
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGTAATCCCAGCACTATGGGAGGCCAAGGTGG
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCCGTGTCTCTACT
AAAAATACAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGA AAAACATCCTCATGGCCACAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGT
AATATAATATTACATGCCACTAAAAAGATAAGGTAGCTGTATATTTCTGGTATGGAAAAA
CATATTAATATGTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGCCATTGAAA
TGGCATTGAAATAAAAGTGTAAGAAATCTATAACAGATGTAGTAACAGTGGTTTTGGGCTG
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGTATTTCTATAATGTTTGAATTTGT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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FIGURE 414

MRLIRNIYIFCSIVMTAEGDAPELPEEREIMTNC SNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLPIIN
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFIQ
QDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLPHLKTLI
LNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENC SWPETVVMNLSYNKLSDSVFRCL
PKSIQILD LNNNQIQTVPKETIHLMALRELNIAFNFLTDLP GCSHF S RLSVLNIEMNFILSPS
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLE TYSEVMVGWSDSYTCEYPLNLRGTRLKDV
HLHELSCNTALLIVTIVIMLV LGLAVAFCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

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FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCGGGGCGCGGGCCGAGCCACCTCTTCCCTCCCCCG
TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCAGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGCGCGGGACGGAGAGAAAACAACTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCGCGGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCCTGGTCCGGGACAGCCGACCTCCCTGCCAAGTGCACCTGGCTCATCTGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCTGAGGAAG
AGTTTCAGTGCCTGAACCACCGCTGTGATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCTCCTGCTTGCATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGCTGGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG
GAGATGCACTGCATGTGTATGACGGCCCTGGGCCCTGAGAGCTCCGACTACTGCGTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGCTTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGTACAGTGAAGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGGCTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTCCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCCACCC
CTTCTACGGGCAGCTCATTTGCCAGGGTGCCATCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
ACTCAGTGTGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTTGCTCCCTCGAA
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTGACACCTTCTGCTGCTCCCCTTGAGGCCCTAGATG
GTGGCACAGTCCAGCCGTGAGGGCGGGGCAAGATGGGGAGCAGGACACCCCACTGCCATCA
AGGCTCCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCCTCC
ACCACTTCCCTTCCCTGTCCCTGGATTTGAGGGACTTGGTGGGGCTCCCGTTGACCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACTGCTCCCCACGCCACCACCTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCCAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

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FIGURE 416

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVOGTLQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDIFYGVFSSPGYTHLASVSHQPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVHVYDG
PGPPSSRLLRSLTHFSNGKAVTVETLSGQAVVS YHTVAWSNGRGNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRCDKCVYETWVCDGQPD CADGSDEWDCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVRRLLRRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGFPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 417

GTGTTCTCCTTTGCTCTCTCGCGCCCAAGTCCTCTCCTCGTTTCTCCTCAGCCGCTGTCCGAGGAGAGACACCCGGA
GACGCGGGCTGCAGTCGCGGCGGGCTTCTCCCCGCCTGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCCCTAG
AGCCTCCCTTGC CGCCTCCCTCCTCTGCCCGGGCCGACAGCATGTCATGGGGTGTGGAGGGTAGATGGGCTCCCG
GCCCGGAGGCGGCGGTGGATCGGGCGCTGGGCAGAGCAGCGCCGATTCAGACTGCCCCGCGCGCCCGGGCG
CCCTTCGAGTCCCCGGTTAGCCATGGGGACCTCTCGAGCAGCAGCACCGCCCTCGCCTCTCGACGCCGCATC
GCCCGCGAGCCACAGCCACGATGATCGGGGCTCCCTTCTCCTGCTTGGATTTCCTTAGCACCAACACAGCTCAG
CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAAGTGTCAGCAGGAACCTATGTCTCTGAGCAATTGTACCAACACAAGCCTGCGCGCTCTGCAGCAGTTGCCCT
GTGGGAGCTTTACAGGCATGAGAATTGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATG
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAAATGCACCTTGCCCACTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATAACGGTGTGCTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAGCATACACAGACTGT
CTGAGTCAGAACCCTGGTGGTGATCAAGCCGGGACCAAGGAGACAGACAACGCTGTGTGGACACATCCCGCTCCTTC
TCCAGTCCACCTCACCTTCCCTCCCTGGCACGCCATCTTTCCAGCCCTGAGCATGGAACCCATGAAGTCCCT
TCTCTCCACTTATGTTCCCAAAGGCATGAACCTCAACGAATCCAACTCTTCTGCTCTGTTAGACCAAAGGTACTG
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCCTC
CCAAACCTTCAGTGTGTCACACCACAGCAAGGCCCCACCACAGACACATCCTGAAGTGCTGCCGTCCATGGAG
GCCACTGGGGGCGGAAGTCCAGCAGCGCCCATCAGGGGCCCAAGAGGGGACATCCTAGACAGAACTACACAAG
CACTTTGACATCAATGAGCAATTTGCCCTGGATGATTGTGCTTTTCTGCTGTGTGCTGTGGTGTGTTGTTG
TGCAGTATCCGGAAGGCTCGAGGACTCTGAAAAAGGGGCCCGGCAGGATCCCAGTGCCATTGTGGAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAGATATCTAGTTTCTTTGCAATGCCAGTGAG
AGGGAGGTTGCTGCTTTCTCCATGGGTACACAGCCAGCAGCAGCGGGCCTACGCAGCTCTGCAGCATGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAAATTAGCGCCTGCGCCAGCAGCCGGAACCATGTTGTGTGAG
AAGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAACCTGACAACTAGCTCTCCCGATGAGCCCCAGCCCC
CTTAGCCCCGAGCCCCATCCCAGCCCCAACCGCAAACCTTGAGAATTCGGCTCTCCTGACGCTGGAGCCTTCCCCA
CAGGACAAGAACAAAGGGCTTCTTCGTGGATGAGTCGGAGCCCTTCTCCGCTGTGACTCTACATCCAGCGGGCTCC
TCCGCGCTGAGCAGGAAGGTTCTTTATTACCAAGAAAAGGACACAGTGTGTGGCAGGTACGCCCTGGAC
CCGTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
ATTCCCCAGGCTGAGGACAAACTAGACCGGCTATTGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAATTAATCTCA
ATTTAGTGGCAGGGTGTTTTTAAATTTCTCTGTTTTCTGATTTTTGTTGTTGGGGTGTGTGTGTGTGTTGT
GT
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAGCCTTTGCCAGGTGTAAGTGTGTGAA
ATACCCACCACTAAAGTTTTTTAAGTTCATATTTTCTCCATTTTGCCCTCTTATGTATTTTCAAGATTATTTCTG
TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACATGGATTGTGAGGCTCTTAAC
TTCTTTAAAGTATAATGGCATTTTGTGAATCTATAAGCAGCTTTTATGTCTTTAATCTTCAACATTCACACTTTT
AAAAACAATATATTACTATTTTATTATTTGTGCTTTTAAATTTTCTTAAAGATTAAAGAAATTAAGA
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTATATTTCTG
CTGAAACTTGACCACACTATTGCTGATGTATGTTTTACCTGGACACCGGTGTAGAATGCTTGATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCT
GACAACGGGCCACCAAGAACTTTGAACCTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTGTGCTTTAAAGATGTCTGT
TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTTGGTCTGGTGGGATTCTTCAACCAAT
ACTTTAATTAATAATGGCTGCAACTGTAAGAACCCTTGCTGTATATTTGCAACTATGCTCCCATTTACAAATG
TACCTTCTAATGCTCAGTTGCCAGTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAACATTAGGTGTTTGTTA
AAAAA

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FIGURE 418

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLGLFLSTTTAQPEQKASNLIQTYRHVD RATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLP CAAL
TDRECTCPPGMFQSNATCAPHTVCPVGVGVRKKGTE TEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGT AIFPRPEHMETHEVPSSTYVPKGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTL PNLQVNVNHQQGPHHRHILKLLPS
MEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVI VVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVA AQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHW TIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL
ETDKLALPMSPLSPSPPIPSNAKLENSALITVEPSPQDKNKGFFVDESEPLLRCDSTSSGS
SALSRNGSFITKEKKD TVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

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FIGURE 419

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCGACTCCACCAATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
GAGGCTTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTGCGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAGAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCTTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCACGCTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCACTTCTTACCCTCTACATCAGTCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCACTGCTGGGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAAGTGGGGATGCTGCTGGGTGGGCGGCCCACTCCACGAGG
GAGCAGATGCGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCAGAGTCCCCAGGACCGCGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTGTGCTGCTCACCATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGCAAAGCAAAGAAATGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAACATGTTGAATTTGTACAACCTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCAAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGGCATC
GGTGTGCTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
GCTGCCATACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCTGTTGGGATTGCCCAGGTGTTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG
CACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGTCTTGGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCAGAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
TGCCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT
GCCTGGAAGAGGTCTGGGTGGGAGGCCAGTCCCATAGGAAGGAGTCTGCC

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FIGURE 420

MNVALQELGAGSNVGFQKGTROLLGSRTQLELVLAGASILLALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLEFLPSRDYYLNRTANEKVLTAAYLDYM
EELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLELSDSEPVVVYGM DYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLDRRFES
AQEKLETLTGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAF
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY
NFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:
amino acids 32-57

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FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC
GCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCCTGGCAGTGCTGGTGCCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA
GAAGATCCGGCACACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC
GCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCCACGT
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA
GGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCCGCCCCCTCGGGAAT
CACAACCTGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTACAGCTGAGCTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTGCTGG
GCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCCGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCGGGACCCCCCTGCCTTCCTGC
TCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAA

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FIGURE 422

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY
KTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGATC
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCTGGATGCT
GCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAACCTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACTCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAAGATTA
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCTGGAA
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCCTTCTTTTCCTT
TTTCTTCACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 424

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD

ADLACQKRPSGKLVSVLSGAEGSFVSSIVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD

VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:**Signal peptide:**

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 425

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTGG
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC
AACATCCGGGGCAAACCTGGTGTGCTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGCGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTAACTGCTCGCCTTCCCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCTCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAACTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTTATAAACCACCGCGTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCTAGGCAGTGCCAGCCAAATAGGAGGCATTC
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAAACAATACCTCACGATATA
AAATAAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVNVASECGFTDQH
YRALQQLQORDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTSKGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT
AAGGTTTCATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTGTTTATCTTCACTA
TTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCTGACACATTTATGTAGTGATCCCACAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAAGTTTGT
AGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 428

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCAGGCAAATGGTGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT
GTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATAACACCTGGGTCAAG
TACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAAGTCAAATTAAATTCTTCCCAATGCCCCAACTAATTTTGAGATTTCAGTCAGAAAATA
TAAATGCTGTATTTATA

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FIGURE 430

><ss.DNA57834
><subunit 1 of 1, 176 aa, 1 stop
><MW: 19616, pI: 7.11, NX(S/T): 0
MVLTIQSHGYEVFNIISSPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIV

Important features:**Signal peptide:**

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

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FIGURE 431

GCCTGGGGATGTCTAGGAGCTCGAAGGTGGTGGTGGGCCTCTCGGTGCTGCTGACGGCGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTATTT
TGA CTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAATCAT
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTTGGAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 432

MSRSSKVLGLSVLLTAATVAGVHVKKQWDQORLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

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FIGURE 433

GAATTCGTGCTCTCGGCACCTCACTCCCGGCCGCCCGGACAGGGAGCTTTTCGCTGGCGCGCTTGGCCGGCGACAGGA
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC
CGCTGCCGTGCTGCTGGGCCCTCTTCTCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGGAAGAAGCCA
AGCCTTACC CGCTATTCCCGGGACCTTTCCAGGGAGCCTGCAAACTGACCACACACCGCTGTTATCCCTTCCTC
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTCAACAACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT
CCCCAGGTGACCTCTGTGGAATCAAAGCCCCCTACCGCCTCTTGCCCTTCAAACACACAGTTGGACACATAATACTT
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG
TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTTTATCCAGATGATGAAGTTACAGCA
ATAATCGCTTCCTTCAGCATAACCAGTGTGCAGCGTTAGACAAATGGGTGCTATATCTGTAAGATGAAAATAAAC
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCCTCACTTTACTAAGCAGCCTGAGAGC
ATGAATGTCAACCAGAAACACAGCCTTCAACCTCACCTGTCAAGGCTGTGGCCCCGCTGAGCCCCGTCAACATTTTC
TGGGTTCAAACACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCCGGCGTGTCTAACTGTTCCAGGCCTGACG
GAGATGGCGGTCTTCAGTTGTGAGGCCCAATGACAAAGGGCTGACCGTGTCCAGGGAGTGCAGATCAACATC
AAAGCAATTCCCTCCCCACCACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT
CCTGGTTTTGATGGATACTCCCGTTCAGGAATTGCAGCATTCAAGTCAAGGAAGCTGATCCGCTGGGTAAATGGC
TCAGTCATGATTTTTAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
AGCATTTGGTGTTCCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCACAGCTGAA
GGAGCCCCATCAGTAGCACCTTTAAATGTCACTGTGTTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
ATGAAGCTCCGACTAAGCAGCAGGATGGAGAACTGGTGGGCTACCGGATATCCACGTGTGGCAGAGTGCAGGG
ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
ACGTGCACAGTGAAGATTGCAGCCGTCAACAGAGGGGGAGTTGGGCCCTTCAGTGATCCAGTGAATAATTTATC
CCTGCACACGGTTGGGTAGATTATGCCCTCTTCAACTCCGGCGCCTGGCAACGCAGATCCTGTGCTCATCATC
TTTGGCTGCTTTTGTGGATTATTTTGTGTTGTTGTTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTATATAGCAAAGAAATCCTTC
TGTCGGCGAGCCATTGAACCTTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAAGTAGAAGATGTT
GTGATTGACAGGAATCTTCTAATTCTTGGAAAAATCTGGGTGAAGGAGAGTTTGGGCTGTGAATGGAAGGAAT
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACTCTTCACTCGGGAG
ATCGAGGAGTTTCTCAGTGAGGCAGCGTCATGAAGACTTCAGCCACCCAAATGTCACTTCTAGGTGTG
TGTATAGAAATGAGCTCTCAAGGCATCCCAAGCCCATGGTAATTTTACCTTTCATGAATACGGGGACCTGCAT
ACTTACTTACTTTATCCCGATTGGAGACAGGACCAAGCATATTCCTCTGCAGACACTATTGAAGTTCATGGTG
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTAGCTGCTCGAAACTGCATG
TTGCGAGATGACATGACTGTCTGTGTTGCGGACTTCGGCTCTCTAAGAAGATTTACAGTGGCGATTATTACCGC
CAAGGCCGATTGCTAAGATGCCTGTAAATGGATCGCCATAGAAAGTCTTGCAGACCGAGTCTACACAAGTAAA
AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCGAAGACTGCCTGGATGAAGTGTAT
GAAATAATGTACTCTTGCTGGAGAACCAGTCCCTTAGACCGCCCCACCTTTTCACTATTGAGGCTGCAGCTAGAA
AAACTCTTAGAAAGTTTGCTGACGTTCCGAACCAAGCAGAGCTTATTTACGTCAATACACAGTTGCTGGAGAGC
TCTGAGGGCCTGGCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCTGACTCTATAATTGCCTCC
TGCACTCCCCGCGCTGCCATCAGTGTGCTCACAGCAGAAGTTCATGACAGCAAACTCATGAAGGACGGTACATC
CTGAATGGGGGAGTGAAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCACAGCTGAAAAGAACAGT
GTTTTACCGGGGGAGAGACTTGTTAGGAATGGGGTCTCCTGGTCCCATTCGAGCATGCTGCCCTTGGGAAGCTCA
TTGCCCGATGAACTTTGTGTTGCTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA
GACATTCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGTCTT
CCTTACCAAGTGAACCTCATGGCCCCAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAAATACATAA
TATATATTTATTTAAAGAGAAAAATATGTGTATATCATGAAAAAGACAAGGATATTTTAAATAAACATTACTTA
TTTCATTTCACTTATCTTGATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
AAGTTGTTTTTTCAACTTCTTTTCTTTTTCATTACTATTAAATGTAATAATTTGTAAATGAAATGCCATATT
TGACTTGGCTTCTGCTTGTATTTGATAAGAAATGATTAATTTTCTGATATGGCTTCCATAATAAATTTGAA
ATAGGA

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FIGURE 434

MGPAFLPLLLGLFLPALWRRRAITEAREEAKPYPLFPFPGSLQTDHTPLLSLPHASGYQPALMFSPTQPGRPHT
 GNVAIPQVTSVESKPLPPLAFKHTVGHILLSEHKGVKFNCSINVPNYQDTTISWWKDGKELLGGHHRITQFYPD
 DEVTALIASFSITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE
 PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCAANDKGLTVSQGVQINIKAI PSEPTEVSIRNSTAHSI
 LISWVPGFDGYSFPRNCISIQVEADPLGNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL
 ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQODGELVGYRISHVWQSAGISKELLEVEVGQNGSRARISV
 QVHNATCTVRIA AAVTRGGVGPFSDPVKIFIPAHGWVDYAPSSTPAPGNADPVLIIFGCFCGFI LIGLILYISLAI
 RKRVTQETKFGNAFTEEDSELVNYIAKKSFCRRAIELTLHSLGVSEELQNKLEDVVIDRNLILGKILGEGEFGS
 VMEGNLQEDGTSILKVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGIPKPMVILPFMK
 YGDLHTYLLYSRLETGPKHIPLQTLKFMVDIALGMEYLSNRNFLHRDLAARNCMRLDDMTVCVADFGLSKKIYS
 GDYYRQGRIAKMPVKWIAIESLADRVTYSKSDVWAFGVTMWEIRTRGMTYPYGVQNHEDYLLHGHRLKQPEDC
 LDELYEIMYSCWRTDPLDRPTFSVLRQLQLEKLLSLPDVRNQADVIVNTQLLESSEGLAQGPTLAPLDLNDP
 SIIASCTPRAATSVVTAEVHDSKPHEGRYILNGGSEEWEDLTSA PSAAVTA EKNSVLPGERLVRNGVSWSHSSML
 PLGSSLPDELLFADDSSEGSEVIM

Signal sequence:

Amino acids 1-18

Transmembrane domain:

Amino acids 501-520

N-glycosylation sites:

Amino acids 114-118;170-174;207-211;
 215-219;234-238;294-298;316-320;329-333;
 336-340;354-358;389-393;395-399;442-446;
 454-458;625-629

Tyrosine kinase phosphorylation sites:

Amino acids 675-683;865-873;923-930

N-myristoylation sites:

Amino acids 41-47;110-116;171-177;
 269-275;275-281;440-446;507-513;535-541;
 966-972

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 351-362

Tyrosine protein kinases specific active-site signature:

Amino acids 719-732

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FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCACTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTTCAGTGTCCGATTCTGATTCCGGCAAGGAT
CCAAGC**ATG**GGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCTCTG
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCTCCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT
CCCTATGGAAGTAGACATATTGCCTTGTCTTAAAGGTCCTGATCACTTATATCTGGAAACC
AAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTTCCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTTCATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGCATCCAG
AGCCGGGCAGTTTCTCTGTGTGGAGGAGACATCCAGGGGCATGTCACTTCAGTGGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTGGACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCAAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAAACCCAAAGAGAAAACCTTCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTGTCAGAGGAG
CCCTCG**TAA**GTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

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FIGURE 436

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRLSS
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQAK
GTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDHLYLETKTLQGTKGENSLSSTGTFLVDNS
SVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPSCSATCGG
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPASPADGYKQIMPYDLYHPLP
RWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKKLPVEAK
LPWFKQAQEELEEGAAVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTACAGGACATTTCGC
CCCTGTGTGCCACCAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAGGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAACTAACA
ATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA